Run

92:

Title:

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Minimum DB
Maximum DB
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Maximum Match
Listing first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          d. No. is the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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121.505 Million cell updates/sec
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Copyright (c) 1993 - 2004
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A372666
S28055
A37266
S25266
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A55149
S60354
B29806
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Compugen Ltd
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                                    hypothetical prote rhodopsin homolog type II site-speci translation elonga glycoprotein H-a - 5-aminoimidazole r COI intron 16 prot peptidyl-dipeppida NADH2 dehydrogenas Ig heavy chain CRD neuromedin K - pig ranatathykinin C - tetracenomycin A2
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e antigen p20e pre
alpha-myosin heavy
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polyphosphate-gluc
chlorophyll a/b-bi
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pilE protein - Esc
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Ig heavy chain C
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                                                                                                                                                                                                                                                                                                          DNA
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Eur. J. Biochem. 205, 341-345, 1992
A;Title: Placental alkaline phosphatase has a binding site for the human immunoglobulin.
A;Reference number: S21205; MUID:92209522; PMID:1555592
A;Accession: S21205
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-12 <MAK>
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
A58718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig heavy chain V region - human (Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996 C;Accession: S21205
      RESULT :
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JN0026	PH1618	JS0316	T14906	A20186	I41235	PH1189	PH1187	PH1190	C60529	S71034	G49410	S25485	S41909	PH0924	PH0904
sperm-activating p	Ig H chain V-D-J r		al pro	ü		۲,	Ψ.	•	hemocyanın 1 - gre	in - Sa	t-complex polypept	transcription fact	hypothetical proce	T-cell receptor be	l receptor

ALIGNMENTS

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Carnocin UI49 - Carnobacterium sp. (fragment)
C;Species: Carnobacterium sp.
C;Date: 23-Uan-1998 #sequence_revision 30-Jan-1998 #text_change 30-Jan-1998
C;Accession: A58718
C;Accession: A58718
R;Stoffels, G:, Nissen-Meyer, J:; Gudmundsdottir, A.; Sletten, K.; Holo, H.; Nes, R;Stoffels, G:, Nissen-Meyer, J:; Gudmundsdottir, A.; Sletten, K.; Holo, H.; Nes, Appl. Environ. Microbiol. 58, 1417-1422, 1992
A;Title: Purification and characterization of a new bacteriocin isolated from a Call, Reference number: A58718; MUID:92321768; PMID:1622206
                                                                                                                                             A;Status: preliminary
A;Molecule type: protein
A;Residus: 1-7 <5TO>
C;Keywords: antibiotic; lanthionine
                                                                                                                                                                                                                    A;Accession: A58718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EVOLVESGG 9
                             3 SEIQ 6
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                                                                                           Similarity
SEIQ 5
                                                                           Conservative
                                                                 30.5%; 5c.
100.0%; Pr/
0;
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Pred. No. 6.5e+02;
3; Mismatches 2
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2.8e+05;
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R;Takahashi, K.; Kishimoto, S.; Ohori, K.; Yoshizawa, H.; Machida, J. Immunol. 147, 3156-3160, 1991
A;Title: Molecular heterogeneity of e antigen polypeptides in sera A;Reference number: A46453; MUID:92013147; PMID:1717588
A;Accession: B46453
                                                                                                                           A;Experimental source: subtype adr
A;Note: sequence extracted from NCBI backbone (NCBIP:60243)
F;1-10/Domain: signal sequence (fragment) #status predicted <8IG>
                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <TAK>
                                                                                                                                                                                                                                                                                                                                                                      C;Species: hepatitis B virus, HBV
A;Variety: subtype adr
C;Date: 18-Jun-1993 #sequence_revision 08-Nov-1996 #text_change 15-Aug-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
B46453
                                                                                                                                                                                                                                                                                                                                                                                                                                               e antigen p20e precursor - hepatitis B virus (subtype adr) (fragment) N;Alternate names: HBe antigen precursor N;Contains: e antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sperm-activating peptide (Tyr-2, Asn-3, Gly-5, Ile-9, Asp-10 SAP-I) - slate-pencil urch: C;Species: Heterocentrotus mamillatus
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
C;Accession: A60589
R;Yoshino, K.I.; Kajiura, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamagua Comp. Biochem. Physiol. B 94, 739-751, 1989
A;Title: A halogenated amino acid-containing sperm activating peptide and its related potus nudus, Echinometra mathaei and Heterocentrotus mammillatus.
A;Reference number: A60527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: protein
A;Residues: 1-10 <YOS>
C;Superfamily: unassigned animal
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A;Note: the protein is designated as mitochondrial ribosomal C;Keywords: mitochondrion; protein biosynthesis; ribosome
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A; Accession: S78420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ribosomal protein RL41, mitochondrial [validated] - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jul-2000
C;Accession: S78420
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75.0%;
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1; Mismatches
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Pred. No. 2e+03;
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Pred. No. 2.8e+05;
0; Mismatches 1
                                                                      DB 2; Length 10; 2e+03;
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A37268

A37268
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-10 <RUF:
                                                            R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R. J. Biol. Chem. 266, 6607-6613, 1991
A;Title: Heavy and light chain variable region sequences and A;Reference number: A38740; MUID:91177923; PMID:1706720
A;Accession: A37268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Genome: chloroplast
C;Superfamily: cytochrome b559 component F
C;Keywords: chloroplast; photosynthesis; photosystem II; thylakoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Kuntz, M.; Camara, B.; Weil, J.H.; Schantz, R. Plant Mol. Biol. 20, 1185-1188, 1992
A;Title: The psbl. gene from bell pepper (Capsicum annuum): plastid RNA editing also occu A;Reference number: S28055; MUID:93099270; PMID:1463853
A;Accession: S28055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-10 < KUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytochrome b559 component psbF - pepper chloroplast (fragment) c;Species: chloroplast Capsicum annuum (pepper) C;Date: 17-Apx-1993 #sequence_revision 17-Apx-1993 #text_changC;Accession: $28055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Friedman, D.J.; Umeda, P.K.; Sinha, A.M.; Hsu, H. Proc. Natl. Acad. Sci. U.S.A. 81, 3044-3048, 1984 A;Title: Characterization of genomic clones specifying A;Reference number: I46888; MUID:84221901; PMID:6328491 A;Accession: I46868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: psbF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alpha-myosin heavy chain - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997
C;Accession: I46868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-7 < FRI>
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Best Local
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Pred. No. 3.1e
3; Mismatches
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coat protein beta chain, Golgi-derived - rabbit (fragment)
N,Alternate names: beta-COP protein
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 19-Mar-1997 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999
C;Accession: S13636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 placental lactogen-I precursor - mouse (fragment)
C;Species: Mus sp. (mouse)
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 12-Aug-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: A coat subunit of Golgi-derived non-clathrin-coated vesicles A;Reference number: S13636; MUID:91101693; PMID:1898984 A;Accession: S13636
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Nature 349, 215-220, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: A47364
R;Shida, M.M.; N9, Y.K.; Soares, M.J.; Linzer, D.I.
Mol. Endocrinol. 7, 181-188, 1993
A;Title: Trophoblast-specific transcription from th
A;Reference number: A47364; MUID:93225959; PMID:846
A;Accession: A47364
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A;Residues: 1-9 <SER>
C;Superfamily: coattomer complex beta chain
C;Keywords: Golgi apparatus; protein transport
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                                                                                                                                       pilE protein - Becherichia coli (fragment)
C;Species: Bscherichia coli
C;Date: 28-May-1993 #sequence_revision 28-May-1993 #text_change 11-Jun-1993
C;Accession: $25266
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A; Residues: 1-10 < RES>
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Best Local S
Matches
                                     Dupuy, B.; Taha, M.K.; Possot, O.; Marchal, C.; Pugsley, A.P. ol. Microbiol. 6, 1887-1894, 1992
[Title: Pulo, a component of the pullulanase secretion pathway Reference number: $25266; MUID:92374839; PMID:1354833
[Accession: $25266]
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  ;Molecule type: protein
;Residues: 1-7 <DUP>
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1; Mismatches
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Pred. No. 4.9e+03;
1; Mismatches 2;
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Pred. No. 2.8e+05;
3; Mismatches 2;
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PMID:8469232
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N-methylpurine DNA glycosylase - mouse (fragment)
(/Species: Mus musculus (house mouse)
(/Species: Mus musculus (house mouse)
(/Accession: A56029
R;Roy, R.; Brooks, C.; Mitra, S.
Biochemistry 33, 15131-15140, 1994
A;Reference number: A56029; MUID:95092772; PMID:7999773
                                                                                                                                                                                         RESULT 14
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RESULT 12
S29735
                                                                                                                                                                                                                                                                  chlorophyll a/b-binding protein 31K - green alga (Dunaliella tertiolecta) N;Alternate names: photosystem II light-harvesting chlorophyll 31K protein (;Species: Dunaliella tertiolecta C;Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 24-Nov-199 C;Accession: PW0002 R;LaRoche, J; Bennett, J.; Falkowski, P.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R:Phillips, N.F.B.; Horn, P.J.; Wood, H.G. Arch. Biochem. Biophys. 300, 309-319, 1993
A;Title: The polyphosphate- and ATP-dependent glucokinase A;Reference number: S29735; MUID:93143332; PMID:8380966
A;Accession: S29735
                                                                                                                                                                                                   Gene 95, 165-171, 1990
A;Title: Characterization of a cDNA encoding for the 28.5-kDa LHCII apoprotein A;Reference number: JW0040; MUID:91065528; PMID:2249775
A;Accession: PW0002
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PW0002
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A;Molecule type: protein
A;Residus: 1-7 cHH2
C;Keywords: phosphotransferase
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A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <ROY>
                                                                                         Query Match 25.4%; Score 15; DB 2; Length 10; Best Local Similarity 50.0%; Pred. No. 7.6e+03; Matches 3; Conservative 2; Mismatches 1; Indels
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                                           5 NLSHIQ 10
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.6 pugen Ltd.		<pre>September 5, 2004, 09:27:07 ; Search time 6.5 Seconds (without alignments) 96.130 Million cell updates/sec</pre>
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US-09-730-174A-3 59 1 SVSEIQLMHNLG 12 Title: Perfect score: Sequence:

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

501 141681 segs, 52070155 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 12

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	c c	P36960 carnobacter	67 ca	.57 c	10 fusarium	46	50	37	31	14	88	321	52	81 macr	.40 mu	P81822 carcinus ma	53	390 rana	392	146 b	245 1	246 1	76 c	903	251 t	143	988 1	352 c	591 p	395 b		359	290	0.2
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9 1 FIBB_PAPHA 9 1 RE42_LITRU 10 1 GLEM_HUMAN 10 1 GON1_CLUPA 10 1 GON2_CHEPR 10 1 HTF_ROMNI 10 1 HTF_HELZE 10 1 TKNB_RANNI 11 1 CXL1_COUMR 11 1 GXL1_COUMR 11 1 HS70_PINPS 12 1 HEP1_BACSE	
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ALIGNMENTS

NG CO	RN 11. SEQUENCE. RX MEDLINE=92321768; PubMed=1622206; RA MEDLINE=92321768; PubMed=1622206; RA Nes I.F.; RT "Purification and characterization of a new bacteriocin isolated from RT a Carnobacterium sp.", RA Appl. Browner M. Serobiol. 58:1417-1422(1992). C1. FUNCTION: Lanthionine-containing peptide antibiotic (lantibiotic). CC Active on Gram-positive bacteria. KW Antibiotic; Bacterioin; Lanthiotic. MATHIBIOTIC (lantibiotic). SQ SEQÜENCE 7 AA; 786 MW; 741776D05B05BB10 CRC64;	Query Match 30.5%; Score 18; DB 1; Length 7; Best Local Similarity 100.0%; Pred. No. 1.46+05; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps Qy 3 SEIQ 6 Db 2 SEIQ 5	RESULT 2 PSBF CAPAN ID

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us-09-730-174a-3.closed.rsp

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STANDARD;
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P35946;
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Best Local S
Matches 2
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                                                               FUSS FU
P81010;
                       FUSS FUSSO
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                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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InterPro; IPR006216; Cyt_b559.
PROSITE; PS00537; CYTOCHRONE B559; PARTIAL.
Chloroplast; Photosystem II; Heme; Electron transport; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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"The psbL gene from bell pepper (Capsicum annuum): plastid RNA editing also occurs in non-photosynthetic chromoplasts."; plant Mol. Biol. 20:1182-1188 (1992) and reaction and a beta cype cytochrome is tightly associated with the reaction center of photosystem II and possibly is part of the water-oxidation complex.
-!- SUBUNIT: Heterodimer of an alpha subunit and a beta subunit.
-!- SIMILARITY: Belongs to the psbE / psbF family.
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MEDLINE=98054539; PubMed=9392829;
MEDLINE=98054539; PubMed=9392829;
Muve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D., Davey M., East P.D., Thorpe A.;
"Lepidopteran peptides of the allatostatin superfamily.";
Peptides 18:1301-1309(1997).
--- SIMILARITY: Belongs to the allatostatin family.
Neuropeptide; Amidation.
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Badopterygota, Lepidoptera, Glossata, Ditrysia,
Tortricoida, Tortricidae, Olethreutinae, Cydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 17; DB 1; Length 10;
Pred. No. 1.9e+03;
3; Mismatches 2; Indels
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LUMENAL (POTENTIAL).
817D0F59D6D69DC5 CRC64;
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X65570; CAA46539.1; -. PIR; S28055; S28055.
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Matches 3; Conservative
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Matches 2; Conservative
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P82157:
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DOMAIN
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ALL6_CYDDO
ALC P82157;
DT 30-MAY-
DT 30-MAY-
DT 30-MAY-
DT 30-MAY-
DT 30-MAY-
DT CYdiast
CC TOTELT
CC Neoptes
CC TOTELNIN
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REPRESENTATION OF THE PROPERTY OF THE PROP
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LYNFG 7

RESULT 4

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MEDLINE=92268977, PubMed=1588321;

MEDLINE=92268877, PubMed=1588321;

MEDLINE=92268877, PubMed=1588321;

Molecular Characterization of phocine distemper virus: gene order and sequence of the gene encoding the attachment (H) protein.";

J. Gen. Virol. 73:1189-1194(1992).

J. Gen. Virol. 73:1189-1194(1992).

FUNCTION: Probable component of the active polymerase. It may function in mRNA synchesis, capping, methylation and poly(A) synthesis of newly synthesized viral mRNAs, RNA editing of the permitted of the permitter of the perm
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01-JUN-1994 (Rel. 29, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
RNA polymerase beta subunit (EC 2.7.7.48) (Large structural protein)
(L protein) (Fragment).
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                              15-71.1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Allergen Fus s 13596* (Fragment).
Pusarium solani (subsp. pisi) (Nectria haematococca).
Eukaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phocine distemper virus (PDV).
Viruses, sRNA negative-strand viruses, Mononegavirales,
Paramyxoviridae, Paramyxovirinae, Morbillivirus.
NCBI_TaxID=11240,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D10371; BAA01208.1; -.
Transferase; RNA-directed RNA polymerase.

NON TER 10
SEQUENCE 10 AA; 1105 MW; 9C2B7FD452D5A2D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=IARI 3596; TISSUE-Mycelium,
Verma J., Gangal S.V.;
Submitted (JUL-1997) to Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 AA; 898 MW; C372C441F5B69041 CRC64;
8 AA.
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PRT;
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2; Conservative
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PRT;
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PIR; S35490; S35490.
REBASE; 1541; PvuI.
                 Neuropeptide, Amidation.
MOD_RES 11 11
SEQUENCE 11 AA; 1114 MW;
                                                                                        25.4%;
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HYPERNEURAL MUSCLE
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Best Local Similarity
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Best Local (
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TRPI PSEPU
ID TRPI PS
AC P36414
DT 01-JUN
DT 15-MAR
DE HTH-tyl
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TOP PROVE
DT 01-JUL DT 01-JUL DT 01-JUL DT 01-JUL DE TYPE I DE TYPE
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TISSUE=Abdominal perisympathetic organs;
MEDLINE=95232021; PubMed=7716075;
Peredel R., Linde D., Rapus J., Vettermann S., Penzlin H.;
Periviscerokinin (Pea-PVK): a novel myotropic neuropeptide from the perisympathetic organs of the American cockroach.";
Peptides 16:61-66(1955).
-i- FUNCTION: MYOACTIVE PEPTIDE; HAS EXCITORY ACTIONS ON THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
EF-G/F-2 subfamily.
Interpro; IPR000795; GTPbind.
PROSITE, PS00301; EFACTOR GTP; PARTIAL.
Elongation factor; Protein biosynthesis; GTP-binding.
                                                                                                                                                                                                                                                                                                           Clostridium pasteurianum.
Bacterin Pirmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
NCBI_TaxID=1501;
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01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Periviscerokinin-1 (Pea-PWK-1).
Enkaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Orthopteroidea, Dictyoptera, Blattaria, Blattoidea, Platidae, Periplaneta.
Nel TaxiD-6978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.1%; Score 16; DB 1; Length 11; 25.0%; Pred. No. 3.3e+03; tive 3; Mismatches 3; Indels
Length 10;
                                   2; Indels
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   DB 1;
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Pred. No. 3e+03;
2; Mismatches
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MEDLINE=98291870; PubMed=9629918;
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h 27.1%;
Similarity 50.0%;
4; Conservative
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nes 2; Conservative
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                                                                                                            SVSVNQIL 10
                                                                          1 SVSEIQLM 8
   Query Match
Best Local Similarity
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P41837;
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EFG_CLOPA
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an emil to license@isb-sib.ch).
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P36114;
01-UUN-1994 (Rel. 29, Created)
01-UUN-1994 (Rel. 29, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
HTH-type transcriptional regulator trpl (TrpBA operon transcriptional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=ATCC 13315;
MEDLINE=93087186; PubMed=1454536;
Smith M.D., Longo M., Gerard G.F., Chatterjee D.K.;
mith M.D., Longo M., Gerard G.F., Chatterjee D.K.;
mcloning and characterization of genes for the Pvul restriction and modification system.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic Acids Res. 20:5743-5747(1992).
-!- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE CGATCG AND
-:- CLEAVES AFTER T-4.
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give specific double-stranded fragments with terminal 5'-phosphates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1993 (Rel. 26, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Type II restriction enzyme Pvul (BC 3.1.21.4) (Endonuclease Pvul)
(R.Pvul) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Proteus.
NCBI_TaxID=585;
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                                                                                          Score 15; DB 1; Length 11;
Pred. No. 5.1e+03;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Restriction system; Hydrolase; Nuclease; Endonuclease.
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AMIDATION.
39DB5419D7605728 CRC64;
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Query Match
Best Local Similarity 50.0%
    2; Conservative
                                           8 MHNLG 12
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                                                                                      2 MYDFG 6
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P82152;
                                                                                                                                                                                            AL18 CARMA
P81821;
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SEQUENCE
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Best Local
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ALL1 CYDPO
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CARMA
    Matches
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-!- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPBA GENES ENCODING THE TO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE INDUCER (INDOLEGINCEROL PROSPHATE), TRPI BINDS UPSTREAM OF THE TRPAB OPERON, OVERLAPPING ITS OWN PROMOTER REGION.

-!- SIMILARITY: Contains 1 HTH lysR-type DNA-binding domain.
                                        Pseudomonas putida.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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"Lepidopteran peptides of the allatostatin superfamily.";
Peptides 18:1301-1309(1997)
                                                                                                                                                                                                                Eberly L., Crawford I.P.;
"DNA sequence of the tryptophan synthase genes of Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interpro, IPR000847, HTH LysR.
PROSITE, PS50931, HTH LYSR, PARTIAL.
Tryptophan biosynthesis, Transcription regulation, Activator,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Lepidoptera, Glossata, Ditrysia;
Tortricoidea, Tortricidae, Olethreutinae, Cydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23.7%; Score 14; DB 1; Length 6; 40.0%; Pred. No. 1.4e+05; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.7%; Score 14; DB 1; Length 7; 40.0%; Pred. No. 1.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Belongs to the allatostatin family. Neuropeptide; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 AA; 683 MW; 77672AA1EDD6F000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 873 MW; 672879CABB569350 CRC64;
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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                                                                                                                                                                       STRAIN=PPG1 C1S;
MEDLINE=89335826; PubMed=2503057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Larva;
MEDLINE=98054539; PubMed=9392829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cydia pomonella (Codling moth).
                                                                               Pseudomonadaceae; Pseudomonas.
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activator) (Fragment).
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Best Local Similarity
                                                                                                                                                 SEQUENCE FROM N.A.
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MAHDL 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- FUNCTION: May act as a neurotransmitter or neuromodulator.
--- SIMILARITY: Belongs to the allatostatin family.
Neuropeptide, Amidation; Multigene family.
AMIDARES 8 AMIDATION (POTENTIAL).
SEQUENCE 8 AA; 919 MW; C82879D5AB569AB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Cerebral ganglion, and Thoracic ganglion;
MEDINE-89121193; PubMed=9461295;
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
Thorpe A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bükaryöta; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Tortricoidea; Tortricidae; Olethreutinae; Cydia.
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MEDLINE=98054539; PubMed=9392829;
Buve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley
Buvey M., East P.D., Thorpe A.;
"Lepidopteran peptides of the allatostatin superfamily.";
Peptides 18:1301-1309(1997).
-: SIMILARITY: Belongs to the allatostatin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Arthropoda, Crustacea, Malacostraca, malamalacostraca, Bucarida, Decapoda, Plocyemata, Brachyura, Bubrachyura, Portunoidea; Portunidae, Carcinus.
1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.7%; Score 14; DB 1; Length 8; 40.0%; Pred. No. 1.4e+05; tive 2; Mismatches 1; Indels
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8 AA; 934 MW; C82879C45B51F775 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                         Carcinustatin 18. Carcinus maenas (Green crab)
                                                                                                                                                                                                                                                                                                   30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                    B AA.
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2; Mismatches
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2; Conservative
                                                                                                                                                                                                                                                    STANDARD;
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Search completed: September 5, 2004, 09:35:02 Job time : 8.5 secs
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RESULT 15
AL19_CARMA
ID AL19_CARMA
AC P81822;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thorpe A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Fibroblast,
MEDLINE=9500997; PubMed=7523108;
MEDLINE=9500997; PubMed=7523108;
MEDLINE=9500997; PubMed=7523108;
MEDLINE=9500997; PubMed=7523108;
"Separation and sequencing of familiar and novel murine proteins using preparative two-dimensional gel electrophoresis.";
Electrophoresis 15:735-745(1994).
-!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown protein is: 6.0, its MW is: 32 kDa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse),
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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01-OCT-1994 (Rel. 30, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Unknown protein from 2D-page of fibroblasts (P32) (Fragment).
                                                                                                                                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
FMRFamide-like neuropeptide FLP8 (VSHNNFLRR-amide).
Macrobrachium rosenbergii (Glant firsh water prawn).
Bukaryota, Metazoa, Arthropoda, Crustacca;
Bumalacostraca, Bucarida, Decapoda, Plecoyemata, Caridea, Palaemonoidea, Palaemonidae, Macrobrachium.
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GO:0007218, P:neuropeptide signaling pathway; IDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 9 AMIDATION.
9 AA, 1133 MW, 845A0729C44441F5 CRC64;
                                                                         9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21107394; PubMed=11179812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE, AND MASS SPECTROMETRY. IISSUE=Eyestalk,
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Matches 2; Conservative
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MOD_RES 9 9
SEQUENCE 9 AA, 1133 MV
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-I. FUNCTION: May act as a neurotransmitter or neuromodulator.

-I. SIMILARITY: Belongs to the allatostatin family.

MOD RES

BOOUTENTION (POTENTIAL)

MAINTIAN (POTENTIAL)

RESOURT TO AM (101 MW) 96687CD5AB569AB1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Cerebral ganglion, and Thoracic ganglion,
MEDLINE=98121193; PubMed=9461295;
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                                      30-MX-2000 (Rel. 39, Created)
30-MX-2000 (Rel. 39, Last sequence update)
30-MX-2000 (Rel. 39, Last sequence update)
30-MX-2000 (Rel. 39, Last annotation update)
Carcinustatin 19.
Carcinus maenas (Common shore crab) (Green crab)
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae; Carcinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 10;
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40.0%; Pred. No. 7.2e+03;
tive 2; Mismatches 1;
10 A.A.
   PRT;
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nes 2; Conservative
   STANDARD;
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September 5, 2004, 09:30:03; Search time 27.5 Seconds (without alignments) 137.681 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Sequence:
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SPTREMBL 25:* 1: Sp_archea:* 2: sp_bacteria:* 3: sp_fungi:* 4: sp_inverebrate:* 5: sp_inverebrate:* 6: sp_mammal:* 7: sp_mhc:* 10: sp_plant:* 11: sp_organelle:* 12: sp_virus:* 13: sp_vertebrate:* 14: sp_unclassified:* 15: sp_unclassified:* 16: sp_bacteriap:* 17: sp_archeap:* 18: sp_varcheap:* 19: sp_archeap:* 10: sp_archeap:* 11: sp_archeap:* 12: sp_archeap:* 13: sp_archeap:* 14: sp_archeap:* 15: sp_archeap:* 16: sp_archeap:* 17: sp_archeap:* 18: sp_archeap:* 18: sp_archeap:* 19: sp_archeap:* 10: sp_archeap:* 10: sp_archeap:* 11: sp_archeap:* 12: sp_archeap:* 13: sp_archeap:* 14: sp_archeap:* 15: sp_archeap:* 16: sp_archeap:* 17: sp_archeap:* 17: sp_archeap:* 18: sp_archeap:* 18: sp_archeap:* 19: sp_archeap:* 19: sp_archeap:* 10: sp_archeap:* 10: sp_archeap:* 11: sp_archeap:* 12: sp_archeap:* 13: sp_archeap:* 14: sp_archeap:* 15: sp_archeap:* 16: sp_archeap:* 17: sp_archeap:* 18: sp_archeap:* 18: sp_archeap:* 18: sp_archeap:* 19: sp_archeap:* 19: sp_archeap:* 19: sp_archeap:* 19: sp_archeap:* 10: sp_archeap:* 11: sp_archeap:* 12: sp_archeap:* 13: sp_archeap:* 14: sp_archeap:* 15: sp_archeap:* 16: sp_archeap:* 17: sp_archeap:* 18: sp_archeap:*

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	Description	Q9ps71 agkistrodon	P82081 limnodynast	P82082 limnodynast	P82083 limnodynast	P82085 limnodynast	Q34909 locusta mig	092766 canine dist	O71066 canine dist	Q40659 oryza sativ	Q9pxc3 hepatitis b	Q23876 dictyosteli	Q85631 avian carci	Q28742 oryctolagus	Q15891 homo sapien	Q9gd12 linospadix	Q9gcv6 sclerosperm
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ALIGNMENTS

Database :

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date) rata; Eutelecs; Colubroide s; Colubroide and F.S.Jr.; colytic enzyme contortrix CRC64; Length 11; '; Indels	(a
reated) ast sequence update) ast sequence update) e (Fragment). Craniata; Vertebrata; oglossa; Serpentes; Ccrodon. Todon. 7CA02D1D41E8772B CRC64 Score 27; DB 13; Ler Pred. No. 1.4002; i Mismatches 1; 1;	; 12 AA. ed) sequence update)
PRT; 11 13, Created) 21, Last sequence 22, Last sequence 31, Craniata; V SCleroglossa; Ser gkistrodon. =1898066; Henderson G.N., Henderson G.N., Terization of a f ad snake (Agkistr 289:197-207(1991) MW; 7CA02D1D41E8 8%; Score 27; D 4%; Pred. No. 1. 1; Mismatche	PRI Creat Last
MBLrel. MBLrel. MBLrel. alloprot oortrix. contrix. linae; A linae;	Η ΣΣ
SULT 1 QPS71 QPS71; O1-MAY-2000 (TERMBLTE1- Eukaryota; Metallopro Agkistradon contortrix. Eukaryota; Metallopro Lipidosauria; Squamata; Viperidae; Crotalinae; NCBLINE=91308546; PubMe SEQUENCE: MEDLINE=91308546; PubMe Guan A.L., Retzios A.D. "Purification and chara of the southern coppering The southern coppering Arch. Blochen and chara of the southern coppering NOW TER NOW TER SEQÜENCE 11 AA; 1209 Query Match Best Local Similarity 71 Matches 5; Conservativ A FIGHNLG 12	2 82081 82081; 1-MAY-20
RESULT 1099871 1099871 1000 1010 1010 1010 1010 1010 1010 1	RESULT P82081 ID P8 AC P8 DT 0.

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SEQUENCE, AND MASS SPECTROMETRY.
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Matches 4; Conser
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                                    Limnodynastes terraereginae (Northen banjo frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butaleostomi,
Amphibia, Batrachia, Annua, Noobatrachia, Bufonoidea, Myobatrachidae,
Limnodynastinae, Limnodynastes.
                                                                                                                                                                              TISSUE=TIBIAL GLAND;
Raftery M.J., Bradford A.M., Bowie J.H., Wallace J.C., Tyler M.J.;
"Peptides from Australian frogs. The structure of the dynastins from the banjo frogs Limnodynastes interioras, Limnodynastes dumerilii and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Limnodynastes salmini (Salmin's-striped frog).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
Limnodynastinae; Limnodynastes.
NCBI_TaxID=39404;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
Limnodynastinae; Limnodynastes.
[1]
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-I. MASS SPECTROMETRY: MW=772; METHOD=FAB.

SEQUENCE 8 AA; 772 MW; 7B58772455A2C728 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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01-WAY-2000 (TrEMBLrel. 13, Last annotation update)
DYNASTIN 4.
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
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Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
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4; Conservative
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                                                                                                                      NCBI_TaxID=104894;
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Limnodynastes salmini (Salmin's-striped frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Bufonoidea, Myobatrachidae;
Limnodynastinae, Limnodynastes.
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McCracken A., Unlembusch I., Gellissen G.;
McTracture of the cloned Locusta migratoria mitochondrial genome:
restriction mapping and sequence of its ND-1(URF-1) gene.";
Curr. Genet. 11:625-630(1987).
EMBL; X05286; CAA28905.1; --.
GO; GO:0005739; C:mitochondrion; IEA.
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                                                                                                                                                                Similarity 66.7%; Pred. No. 1e+06;
4; Conservative 1; Mismatches 1; Indels
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Last annotation update)
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Locusta migratoria (Migratory locust)
Mitochondrion.
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Alpha-amylase (Fragment).
Oryza sativa (Rice).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta; Liliopsida, Poales, Poaceae; Ehrhartoideae, Oryzeae, Oryza,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE-91078641; PubMed=2258052; MEDLINE-91078641; PubMed=2258052; Mingai M.H., Shah M., Terashima M., Vrkljan Z., Whitaker J.R., Rodriquez R.L.; Expression and secretion of rice alpha-amylase by saccharomycers cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE.

MEDLINE=92013147; PubMed=1717588;

MEDLINE=92013147; PubMed=1717588;

Takahashi K., Kishimoto S., Ohori K., Yoshizawa H., Machida A.,
Ohnuma H., Tsuda F., Munekata E., Miyakawa Y., Mayumi M.;

"Molecular heterogeneity of e antigen polypeptides in sera from carriers of hepatitis B virus.";

J. Immunol. 147:3156-3160(1991).

PIR: B46453; B464453.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
E antigen P202 (Fragment).
Hepatitis B virus.
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
NCBI_TAXID=10407;
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30.5%; Score 18; DB 10; Length 8;
Best Local Similarity 28.6%; Pred. No. 1e+06;
Matches 2; Conservative 5; Mismatches 0; Indels
Query Match 32.2%; Score 19; DB 12; Length 9; Best Local Similarity 100.0%; Pred. No. 1e+06; Matches 3; Conservative 0; Mismatches 0; Indels
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01-NOV-1996 (TrEMBLrel, 01, Last sequence update)
01-OCT-2002 (TrEMBLrel, 22, Last annotation update)
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EMBL; M62916; AAA33892.1;
Gramene; Q40659; -
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1 MQVLNNM 7
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ID Q9PXC3;
DT Q1-MAX-2)
DT 01-MAX-2)
DT 01-MAX-2)
DE B antigel
CS Hepatist;
CS Hitches;
CX NCBL Tax:
RN [1]
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RN EDLINE;
RA MEDLINE;
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RT "MOLECULIMA ANDIGULIMA BET
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STRAIN=Dog #10797/96;
STRAIN=Dog #10797/96;
STRAIN=Dog #10797/96;
"Genetic analysis of the central untranslated genome region and the proximal coding part of the F gene of wild-type and vaccine distemper morbilliviruses.";
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AF026234; AAC09164.1;
SEQÜENCE 9 AA; 1124 MW; F29D04576044041 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

STRAIN=Dog #5556/89;

Liermann H., Harder T., Haas L.;

Liermann H., Harder T., Hass L.;

Liermann H., Harder T.,

Idenetic analysis of the central untranslated genome region and the proximal coding part of the F gene of wild-type and vaccine distemper morbilliviruses.";

Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.

BMBL, AF026237; AAC09167.1; -.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses, ssRnÅ negative-strand viruses, Mononegavirales,
Paramyxoviridae, Paramyxovirinae, Morbillivirus.
NCBI_TaxID=11232;
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Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Morbillivirus.
NCBI_TaxID=11232;
                                                                                                                                                Score 19; DB 8; Length 8;
Pred. No. 1e+06;
2; Mismatches 2; Indels
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Fusion protein (Fragment).
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092766;
01.NOV-1998 (TrEMBLrel. 08, Created)
01.NOV-1998 (TrEMBLrel. 08, Last sequence update)
01.NOV-1998 (TrEMBLrel. 08, Last sequence update)
Fusion protein (Fragment).
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                                                                                          F8E33723304B45B6 CRC64;
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Best Local Similarity 50.0%;
Matches 4; Conservative 5
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8 AA; 1019 MW;
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               Mitochondrion.
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SEQUENCE FROM N.A.
MEDLINE=84221901; PubMed=6328491;
Priedman D.J., Umeda P.K., Sinha A.M., Hsu H.-J., Jokovcic S.,
Rabinowitz M.;
"Characterization of genomic clones specifying rabbit alpha- and beta-
                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M., Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y., Caskey C.T.H.;
"Isolation of chromosome-specific genes by reciprocal probing of arrayed cDNAs and cosmid libraries.",
Hum. Mol. Genet. 0:0-0(1995).
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Arecaceae; Arecoideae;
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Last sequence update)
Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Ribosomal protein S16 (Fragment).
                                                                                                                                                                                                                      1 1 7 AA; 916 MW; 6B1B1AA1E69326B0 CRC64;
                                                                                                                                                      ventricular myosin heāvy chains.";
Proc. Næll Acad. Sci. U.S.A. 81:3044-3048(1984).
EMBL; KOJ698; AAA31415.1; -.
PIR; 146868; 146868.
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01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2011 (TrEMBLrel. 19,
(Clone XP2E8B) (Fragment).
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NON TER 9 9
SEQÜENCE 9 AA, 1030 MW;
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Best Local Similarity 44.4%;
Matches 4; Conservative
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es 3; Conserv
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TISSUE=Placenta;
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SEQUENCE
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Pred. No. 1.1e+04;
                                                                                                                                                                                                                                                                                                                                                                                                             Length 11;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Anian carcinoma virus.
Viruses, Recroid viruses, Retroviridae, Alpharetrovirus.
                                                                                                                                                                                                                                                                       MEDINE=82260445; PubMed=6286214; MCKeown M., Firtel R.A.; McKeown M., Firtel R.A.; Cold Spring Harb. Symp. Quant. Biol. 46:495-505(1982). EMBL, K02957, AAA33150.1; CEBMBL, K02956; AAA33150.1; CEBMBL, K02956; AAA33150.1; GINED.
                                                                                                                                                                    Actin 4.
Dictyostelium discoideum (Slime mold).
Bukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON TER 1 1 1 SEQÜENCE 12 AA; 1466 MW; 72E4B884F30736DB CRC64;
                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TYEMBLrel. 01, Created)
01-NOV-1996 (TYEMBLrel. 01, Last sequence update)
01-UUN-2003 (TYEMBLrel. 24, Last annotation update)
Alpha-myosin heavy chain (Fragment).
Oryctolagus cuniculus (Rabbit).
                                                                                                                                                                                                                                                                                                                                                                                                         Score 18; DB 5;
Pred. No. 1e+04;
4; Mismatches
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100.0%; Pred. No. 1.-
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Best Local Similarity 28.6
Matches 2; Conservative
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                                                                                     PRELIMINARY;
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     1 MQLFH 5
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Q23876;
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Q28742;
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Q85631
ID Q8563:
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Q23876
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Q28742
ID Q2874
AC Q2874
AC Q2874
DT 01-NO
DT 01-NO
DE Alpha
OS Orych
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OC Areceae; Linospadicinae; Linospadix.

NCBI_TAXID=131282;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RA Asmussen C.B., Chase M.W.;
RI Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
RR Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
RR GO; GO:0009507; C:chloroplast; IEA.
RW Chloroplast.
RY Chlor
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Search completed: September 5, 2004, 09:36:59 Job time: 29.5 secs

(0/0/sn) 3U0/8 860/ SIU/

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	OM protein - protein search, using sw model	on: September 5, 2004, 09:26:47; Search time 36.5 Seconds (without alignments) 92.892 Million cell updates/sec	Title: US-09-730-174A-3 Perfect score: 59 Sequence: 1 SVSEIQLMHNLG 12	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	rched: 1586107 segs, 282547505 residues	Total number of hits satisfying chosen parameters: 368311	Minimum DB seq length: 0 Maximum DB seq length: 12
,	OM prot	Run on:	Title: Perfect s Sequence:	Scoring	Searched:	Total n	Minimum Maximum

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SUMMARIES

Description	Aay96968 Parathyro	7 F	щ	4 H	Aay68767 Amino aci	σ.	Abr44166 Human par	Aab86225 Human par		Parath	Aab86220 Human par	Aay50600 Resin bou	Aab01862 PTH(1-14)	Aay96966 Parathyro	Aab01863 PTH(1-14)	Aab96932 Rat parat	Aab96931 Rat parat	Aab96915 Parathyro	Aab84770 Parathyro	Aab96914 Parathyro	Aab84769 Parathyro	Aay78849 Parathyro	Aar91646 Human par	Aab07467 Antigenic	Aab86221 Human par
ID	AAY96968	ABG72607	ABG72608	AAR91644	AAY68767	AAB86219	ABR44166	AAB86225	AAR91645	AAY96981	AAB86220	AAY50600	AAB01862	AAY96966	AAB01863	AAB96932	AAB96931	AAB96915	AAB84770	AAB96914	AAB84769	AAY78849	AAR91646	AAB07467	AAB86221
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Abn71484 Parathyro	ī	Abp71483 Parathyro	ις.	22	Aab01866 PTH(1-14)	Aap82547 (Asn10, T	Aab96892 Rat parat	Aab96891 Rat parat	Aar91647 Human par	Aab86222 Human par	Aab01864 PTH(1-14)	Aay97062 PTH-rP N-	Abg69386 Vascular	Aau93357 Granulocy	Abu54029 Human DNA	Aar89301 Japanese	Aab21270 Fertilin	Aar91648 Human par	Aay68764 Amino aci
ABP71484	ABP71485	ABP71483	AAW45785	ABP71482	AAB01866	AAP82547	AAB96892	AAB96891	AAR91647	AAB86222	AAB01864	AAY97062	ABG69386	AAU93357	ABU54029	AAR89301	AAB21270	AAR91648	AA Y68764
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59.3	59.3		59.3	59.3	55.9	54.2	54.2	4.	50.8		50.8			49.2	45.8	45.8			44.1
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26	27	28	23	30	31	32	33	34	35	36	3.7	38	39	40	41	42	43	44	45

ALIGNMENTS

PTH; parathyroid hormone; N-terminal; signaling domain; bone mass; bone reformation; resorption; remodeling; tether1; osteoporosis. Parathyroid hormone N-terminal signaling domain (residues 1-11). Ä AAY96968 standard; peptide; 11 99WO-US031108. 31-OCT-2000 (first entry) WO200039278-A2. 30-DEC-1999; Homo sapiens. 06-JUL-2000. AAY96968;

98US-0114577P. Σ (GARD/) GARDELLA T J. (KRON/) KRONENBERG H M. (POTT/) POTTS J T. (JUEP/) JUEPPNER H. 31-DEC-1998;

Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;

WPI; 2000-452384/39.

New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass.

Claim 4; Page 92; 119pp; English.

Compounds of the structure or formula S-(L) n-B, R l-S-(L) n-R or S-(L) n-R, are new. S is an amino terminal signaling functional domain of parathyroid hormone (PTH); L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4); B is a C-terminal binding portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R l is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor sequence. The new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone reformation, bone resorbtion and/or bone remodaling, treating diseases and disorders associated with decreased tetherl activity, increasing CAMP

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Gaps

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1; Indels

Mismatches

8X30000

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the method; and (3) test kits and analytical procedures used for the determination of bioactive intact PTH utilising (ab). The methods and compositions of the present invention are useful for determining bioactive intact PTH levels in serum, plasma and/or cell culture media.

The antigens, antibodies and methods of the present invention, as compared to prior art, have the particular advantages of possessing greater affinity for PTH, and in particular, are designed to have a novel recognition for amino acid residues extending beyond the first N-terminal PTH residue, and further have negligible cross-reactivity with the large non-molecular forms of PTH. PTH levels are an important parameter in patients suffering from hypercalcaemia, osteoporosis and primary persent sequence represents a PTH antigenic peptide representing amino acids 2-12 of human, mouse, rat, porcine,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zahradnik RJ, Lavigne JR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-066685/06.
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es 10; Conserv
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Misc-difference 1
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Matches
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               in a mammalian cell having PTH-1 receptors, or screening for a peptide or non-peptide PTH (claimed). The new compound can be administered by inhalation unlike the large nearive PTH or PTHrP which avoids the need for regular injections to treat osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New parathyroid hormone (PTH) antigenic peptide inducing the formation and isolation of antibodies having an affinity to it, useful for determining bioactive PTH levels in serum, plasma and/or cell culture
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                                                                                                                                                            Length 11;
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Pred. No. 0.012;
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90.9%;
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Sus scrofa.
Canis familiaris.
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                                                                                                                       Sequence 11 AA;
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The invention relates to a new antigenic peptide for inducing the formation and isolation of antibodies having an affinity to it, being correct formed from the N-terminus of parathyroid hormone (FTH). Also included are; (1) a method for producing antibodies useful in the determination of FTH levels in a biological sample comprising: (a) providing at least one first peptide antigen comprising a peptide fragment of FTH; (b) administering the first peptide antigen to a host animal to induce antibody production; (c) monitoring the animal; and (e) selecting antisera from the isolated antisera produced in the host three produced; (d) isolating antisera from the isolated antisera produced in the host that is capable of binding to a second peptide antiser, (2) an antibody (ab) produced by the method; and (3) test kits and analytical procedures used for the determination of bioactive intact PTH levels in serum, plasma and/or cell culture media. The antigens, antibodaes and methods of the present invention, as compared to prior art, have the particular advantages of possessing creater affinity for PTH, and in particular, are designed to have a novel croopsition for amino acid residues extending beyond the first N-terminal CTH residue, and further have negligible cross reactivity with the large containts suffering from hypercalcaemia, osteoporosis and primary hyperparathyroidism. The present sequence represents a PTH antigenic peptide representing amino acids 1-12 of human, mouse, rat, porcine, containe and bovine PTH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 50; DB 6; Length 12; Pred. No. 0.014;
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90.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSEIQLMHNLG 12
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12 AA;
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German

Claim 2; Page 4; 5pp;

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Gaps

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                                                 аn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New parathyroid hormone fragment peptides, used as lipolysis stimulants in topically applied cosmetic compositions for slimming treatment of excessive weight in hips and thighs.
The present sequence is a specific example of claimed immunogenic peptides having a sequence from hPTH(1-37) which includes the N- or C-terminal alpha-helical region and/or the non-structured region of the hormone. Antibodies and their binding fragments generated by injecting animal with the peptides are useful as diagnostic reagents for determination of biologically active hPTH(1-37)
                                                                                                                                                                  Gaps
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0.0.017;
0; Indels
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100.0%; Pred. No. 0.017;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                           Amino acids 1-10 of a parathyroid hormone (pTH).
                                                                                                                                                                  Mismatches
                                                                                                                                   10 100.0%; Score 49; Starity 100.0%; Pred. No. Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                    AAY68767 standard; peptide; 10 AA.
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Matches 10; Conserv
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AAB86219;

RESULT 6 AAB86219

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Novel fusion peptide comprising self cell-penetrating Tat peptide bound to human parathyroid hormone-derived peptide, useful as component of skin slimming cosmetic composition.
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                                                                                                 Fusion peptide, tat; hPTHDP; parathyroid hormone; skin; cosmetic; lipolysis; human; hPTH.
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                                                     Human parathyroid hormone (hPTH) fragment (residues 1-10).
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100.0%; Pred. No. 0.017;
iive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cho W, Kang S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GLDS ) LG HOUSEHOLD & HEALTH CARE LTD.
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15-MAR-2002; 2002KR-00014062.
(first entry)
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Matches 10; Conservative
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  04-AUG-2003
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Chang M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB86225;
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100.0%; Pred. No. 0.017;
live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                  Human parathyroid hormone immunogenic peptide SEQ ID 1.
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                                                                                  AAB86219 standard; peptide; 10 AA
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Best Local Similarity 100.
Matches 10; Conservative
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99DE-01061350.

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ABR44166

ABR44166 ID ABR4 XX AC ABR4 XX

RESULT 7

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WO200039278-A2
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                                                                                                                                                                       This invention describes a novel method for determining (M1) the content of active parathyroid hormone (A) by treating a sample with (i) antibody (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A), and including the N-terminal residue and (ii) antibody (Ab2) that recognizes an epitope within the receptor-binding site of (A). The number of molecules that react with both antibodies is determined and used to calculate the content of physiologically active (A). The method is used for diagnosis of calcium-metabolism disorders, osteopathy, or hypo-or hyper-parathyroidism. The method (unlike known assays) recognizes that (B) some fragments of (A) shorter than the complete (B4 aa) peptide are cative and (ii) that apparently intact peptide may be biologically content of inactive, and also takes into account the fact that some fragments of (A) inactive, and also takes into account the fact that some fragments of cerminus). It thus provides a true measure of the content of physiologically active (A); contrast methods that measure intact peptide and its 1-37 fragment which may produce falsely high values. This continue the method of
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                                                                                                Determining the content of physiologically active parathyroid hormone, useful in diagnosis of calcium-metabolism disorders, using two antibodies reactive with different epitopes.
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1.4e+06;
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  99DE-01061350.
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                            (IMMU-) IMMUNDIAGNOSTIK AG
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nes 9, Conservative
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                                                                            WPI; 2001-376318/40.
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                                                      Armbruster FP;
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원 ò

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Compounds of the structure or formula S-(L) n-B, R 1-S-(L) n-R or S-(L) n-R, are new. S is an amino terminal signaling functional domain of parathyroid hormone (PTH); L is a linker molecule present n times (where is a positive integer 1-10 (preferably 4); B is a C-terminal binding portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R.1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor sequence. The new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone reformation, bone resorption and/or bone remodaling, treating diseases and disorders associated with decreased tetherl activity, increasing CAMP in a mammalian cell having PTH-1 receptors, or screening for a peptide or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                            The present sequence is a specific example of claimed immunogenic peptides having a sequence from hPTH(1-37) which includes the N- or C-terminal alpha-helical region and/or the non-siructured region of the hormone. Antibodies and their binding fragments generated by injecting an animal with the peptides are useful as diagnostic reagents for determination of biologically active hPTH(1-37)
New antigenic peptide(s) from human parathyroid hormone - and antibodies generated using them, able to distinguish between active and inactive forms of the hormone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      apound comprising an amino terminal signaling functional domain to a carboxy-terminal binding portion of parathyroid hormone for mammalian conditions characterized by decreases in bone mass.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72.9%; Score 43; DB 2; Length 9; llarity 100.0%; Pred. No. 1.4e+06; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY96981 standard; peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kronenberg HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0114577P
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                                                                                                                                                              Claim 2; Page 4; 5pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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KRONENBERG H M.
POTTS J T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New compound comprising
linked to a carboxv-form
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Best Local Similarity
9, Conserve
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Gaps

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Indels

Pred. No. 1.4e+06; Mismatches 0;

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Conservative

Best Local Similarity Matches 9; Conser

SVSEIQLMH

1 SVSEIQLMH

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100.08;

AAY50600 standard; peptide; 11 AA.

RESULT 12 AAY50600

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Resin bound cyclic peptide 33.

(first entry)

09-FEB-2000

AAY50600;

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This invention describes a novel method for determining (M1) the content of factory parathyroid hormone (A) by treating a sample with (i) antibody (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A), and including the N-terminal residue and (ii) antibody (Ab2) that recognizes an epitope within the receptor-binding site of (A). The number of molecules that react with both antibodies is determined and used to alculate the content of physiologically active (A). The method is used alculate the content of physiologically active (A). The method is used to diagnosis of calcium-metabolism disorders, osteopathy, or hyporolyparathyroidism. The method (unlike known assays) recognizes that (i) some fragments of (A) shorter than the complete (84 aa) peptide are carticle and (ii) that apparently intact peptide may be biologically active, and also takes into account the fact that some fragments of (A) are antagonistic (these have the receptor-binding site but lack the N-terminus). It thus provides a true measure of the content of physiologically active (A); contrast methods that measure intact peptide and its 1-37 fragment which may produce falsely high values. This sequence represents a peptide fragment used to illustrate the method of the content of the invention.
  non-peptide PTH (claimed). The new compound can be administered by inhalation unlike the large native PTH or PTHrP which avoids the need for regular injections to treat osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Determining the content of physiologically active parathyroid hormone, useful in diagnosis of calcium-metabolism disorders, using two antibodies reactive with different epitopes.
                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Parathyroid hormone; hPTH; immunogenic peptide; human; epitope; diagnosis; calcium-metabolism disorder; osteopathy; antagonist; hypo-parathyroidism; hyper-parathyroidism.
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0
                                                                                                                                                         0; Indels
                                                                                                                      Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human parathyroid hormone immunogenic peptide SEQ ID 2.
                                                                                                                  72.9%; Score 43; DB 3; Le 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                 AAB86220 standard; peptide; 9 AA
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(claimed). The
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                                                                                                                                Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                               1 SVSEIQLMH
non-peptide PTH
                                                                            Sequence 9 AA;
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This invention describes a novel method for the preparation of peptides (II) that contain both cyclic and linear peptide fragments comprises sequential reaction of a resin-bound linear fragment with the cyclic ragmential reaction of a resin-bound linear fragment with the cyclic ragment in N-protected form and optionally other linear fragments. The products of the invention have osteopathic and hypotensive activity. (II) bind to hPTH receptors and act as agonists or antagonists of hPTH. The method is particularly used to prepare cyclic peptide analogs of parathyzoid hormone (PTH) or PTH-related peptides which are useful for treating diseases that respond to treatment with agents that bind to PTH receptors (with or without activation of adenyly) cyclase activity), e.g. hyper- or hypo-calcemia, osteoporosis, osteopenia, hyper- or hypo-calcemia, osteoporosis, osteopenia, hyper- or hypo-calcemia, osteoporosis, osteopenia, hyper- or hypo-calcemia, of bone fractures. Separate synthesis of the cyclic for promoting repair of bone fractures. Separate synthesis of the cyclic fragment allows convergent synthesis of resin-bound (II), with better yields and higher throughput. The difficulties associated with preparation of the bridged fragment are confined to a small peptide which
                                                                                                                              Cyclic peptide; resin bound; parathyroid hormone; osteopathic; disease; hypotensive; PTH receptor; treatment; hypor-alcemia; hypo-calcemia; osteoporosis; osteopenia; hypor-parathyroidism; hypo-parathyroidism; cushing's syndrome; renal failure; hyportension; bone fracture repair.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Convergent synthesis of peptides for treating e.g. bone disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (RHON ) RHONE-POULENC RORER PHARM INC.
                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 75; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                "Glu (OtBu) "
                                                                                                                                                                                                                                                                                                      'note= "FMOC-Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "His(Trt)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Asn(Trt)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9952933-A1
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DB 4; Length 9;

72.9%; Score 43;

Sequence 9 AA;

Query Match

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can be purified before reaction with the resin-bound component, AAY50568-
Y50614 represent the peptide fragments described in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        skeletal, neurological system, neuromuscular and cardiovascular systems. It binds to both PTH-1 receptors on osteoblasts and renal tubular cells, and to the recently identified PTH-2 receptor. PTH has a potent anabolic effect on the skeleton, and mediates calcium reabsorption, enhances calcium reabsorption, and mediates calcium reabsorption, and monos calls of prophate clearance and vitamin D synthesis in the kidney. A homologous calls of protein hormones, the PTH-related broteins (PTHFP) mimic some of the renal and skeletal actions of PTH, and also bind to the PTH-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Parathyroid hormone (PTH) peptides, PTH related peptides and the nucleic acids that encode them, useful for treating osteoporosis.
                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Parathyroid hormone peptide; PTH; PTH-related peptide; PTHrP; calcium homeostasis; PTH-1 receptor; PTH-2; vitamin D synthesis; bone synthesis; agonist; osteoporosis; non-parenteral delivery.
                                                                                                             2; Length 11;
                                                                                                                                                0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                          PTH(1-14)/PTHrP(1-14)-derived peptide, SEQ ID NO:6.
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                                                                                                         Score 40.5; DB
Pred. No. 0.73;
L; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 26; 73pp; English.
                                                                                                                                                                                                                                                                                                                AAB01862 standard; peptide; 9 AA.
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                                                                                                           68.6%;
83.3%;
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                                                                                                   Query Match
Best Local Similarity 83.3
Matches 10, Conservative
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KRONENBERG H M.
                                                                                                                                                                                   1 SVSEIQLMHNLG
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JUEPPNER H.
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                                                                        Sequence 11 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                     invention
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(KRON/)
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receptor. They do not bind to the PTH-2 receptor. The peptides of the invention are either agoniets of PTH-1 and PTH-2 receptors (AAB01858, AAB01861-B01866) or are PTH-1/PTH-2 receptor antagonists (AAB01867-B01869). PTH-1/PTH-2 receptor agonists are useful for the treatment of conditions characterised by a decrease in bone mass, such as seteoporosis. PTH-1/PTH-2 receptor antagonists are useful for treatment of nedical disorders that arise from excessive or altered action of the PTH-1/PTH-2 receptor. Detectably labelled peptides of the invention are also useful in the determination of rates of bone formation, bone resorption and/or bone remodelling in a patient. The peptides of the invention are "minimised" versions of PTH or PTH-P which are inexpensive to prepare by conventional synthetic chemistry, and can be delivered to a patient via non-parenteral routes. Sequences AAB01858 and AAB01861-B01866 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Compounds of the structure or formula S-(L) n-B, R 1-S-(L) n-R or S-(L) n-R, are new. S is an amino terminal signaling functional domain of parathyroid hormone (PTH); L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4); B is a C-terminal binding portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R 1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor sequence. The new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone reformation, bone resorption and/or bone remodeling, treating diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New compound comprising an amino terminal signaling functional domain
linked to a carboxy-terminal binding portion of parathyroid hormone for
treating mammalian conditions characterized by decreases in bone mass.
                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTH; parathyroid hormone; N-terminal; signaling domain; bone mae
bone reformation; resorption; remodeling; tether1; osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Parathyroid hormone N-terminal signaling domain (residues 1-9).
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                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                Score 40; DB 3; Length 9;
Pred. No. 1.4e+06;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY96966 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                67.8%;
88.9%;
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                                                                                                                                                                                                                                                                                                                                                                       8; Conservative
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(KRON/) KRONENBERG H M.
(POTT/) POTTS J T.
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                                                                                                                                                                                                                                                                                             Sequence 9 AA;
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and disorders associated with decreased tetheri activity, increasing CAMP in a mammalian cell having PTH-1 receptors, or screening for a peptide or innon-peptide PTH (claimed). The new compound can be administered by inhalation unlike the large native PTH or PTHrP which avoids the need for regular injections to treat osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Parathyroid hormone (PTH) peptides, PTH related peptides and the nucleic acids that encode them, useful for treating osteoporosis.
                                                                                                                                                                                                                                                                                                                          Parathyroid hormone peptide, PTH, PTH-related peptide, PTHrP; calcium homeostasis, PTH-1 receptor; PTH-2; vitamin D synthesis; bone synthesis; agonist; osteoporosis; non-parenteral delivery.
                                                                                              Score 40; DB 3; Length 9;
Pred. No. 1.4e+06;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gardella IJ, Kronenberg HM, Potts JT, Jueppner H;
                                                                                                                                                                                                                                                                                                     PTH(1-14)/PTHrP(1-14)-derived peptide, SEQ ID NO:7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure, Page 26; 73pp; English
                                                                                                                                                                                                                               AAB01863 standard; peptide; 9 AA.
                                                                                                67.8%;
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                                                                                                                                                                                                                                                                             11-SEP-2000 (first entry)
                                                                                                Query Match
Best Local Similarity 88.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GARD/) GARDELLA T J.
(KRON/) KRONENBERG H M.
(POTT/) POTTS J T.
                                                                                                                                              σ
                                                                                                                                                                     1 AVSEIQLMH 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-339693/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (JUEP/) JUEPPNER H.
                                                                                                                                              1 SVSEIQLMH
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                                                                         Sequence 9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                      AAB01863;
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The invention relates to a novel parathyroid hormone (PTH) peptide

(AAB01859) and parathyroid hormone-related peptide (PTHPP) AAB01860), and
biologically active derivatives thereof (AAB01858, AAB01861).

Biologically active derivatives thereof (AAB01851-B01858, AAB01861).

Biologically active derivatives thereof (AAB01857-B01858, AAB01861).

Globaldy The peptide of the invention are at least 85% identical to the generic peptide of the formula: X1-Val-Ser-Glu-X2-Gln-Leu-X3-His-X4-X5-Gly-Leu v7.9 xX6 (AAB01857) where x1 is Ser or Ala; X2 is His or Ser;

Met, Leu or NIe; X4 is Asn or A89; X5 is Leu or Lys; X6 is His or Ser;

provided that the peptide is not PTHPP(1-14). The peptides of the invention active and acides of the invention acides 1-9, 1-10, 1-11, 1-12 and 1-13, and N- and C- terminal derivatives. PTH is a major regulator of calcium homeostasis, and is necessary for the normal function of the gastrointestinal, skeletal, neurological system, neuromuscular and cardiovascular systems. It binds to both PTH-1 receptors on osteoblasts and renal tubular cells, and to the recently identified PTH-2 receptor. PTH has a potent anabolic effect on the skeleton, and mediates calcium reabsorption, enhances

Dhosphate clearance and vitamin D synthesis in the kidney. A homologous

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calls of protein hormones, the PTH-related proteins (PTHrP) mimic some of the renal and skeletal actions of PTH, and also bind to the PTH-1 creeptor. They do not bind to the PTH-2 receptor. The peptides of the invention are either agonists of PTH-1 and PTH-2 receptors (AAB01858, AAB01861) or are PTH-1/PTH-2 receptor antagonists (AAB01867-CC conditions characterised by a decrease in bone mass, such as osteoporosis. PTH-1/PTH-2 receptor antagonists are useful for the treatment of corteoporosis. PTH-1/PTH-2 receptor antagonists are useful for treating medical disorders that arise from excessive or altered action of the PTH-1/PTH-2 receptor. Detectably labelled peptides of the invention are also useful in the determination of rates of bone formation, bone resorption and/or bone remodelling in a patient. The peptides of the invention are minimised" versions of PTH or THYP which are inexpensive to prepare by conventional synthetic chemistry, and can be delivered to a patient via non-parenteral routes. Sequences AAB01858 and AAB01861-B01866 represent
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Best Local Similarity 77.00
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*

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9: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/USO9E_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/USO9E_PUBCOMB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/USO9E_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*

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18: /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-730-174A-3
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US-09-730-174A-6
US-09-730-174A-6
US-108-185-1
US-10-168-185-1
US-10-168-185-7
US-10-168-185-7
US-10-192-673-6
US-10-192-673-7
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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ALIGNMENTS

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US-09-730-174A-5
Sequence 3, Application US/09730174A
Patent No. US2002011087A1
GENERAL INNOGATION:
APPLICANT: Zahradnik, R.J.
GENERAL INNOGATION:
TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having of TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having of TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid HC FILE REFERENCE: INUNB-001A.
TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid HC FILE REFERENCE: INUNBER: US/09/730,174A
CURRENT FILING DATE: 200-12-05
NUMBER OF SEQ ID NOS: 12
TITLE OF INVENTION: Induces Formation of Antibodies and Isolates said Antibodies
CHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-3
OUETY Match
Best Local Similarity 100.0%; Score S9; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00081;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Sequence 5, Application US/09730174A
Application US/09730174A.
GENERAL INVENTION: Abrichedies and Peptide Antigens for Producing Antibodies having if TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid H; FILE REFERENCE: IMUMS-001A
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Sequence 6. Application US/09730174A

Fatent No. US2002110871A1

GENERAL INFORMATION:

APPLICANT: Zahradnik, R.J.

TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Ho;
FILE REPERBNCE: IMUNE-001A

CURRENT APPLICATION NUMBER: US/09/730,174A

CURRENT FILING DATE: 2000-12-05

NUMBER OF SEQ ID NOS: 12

SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09730174A

Sequence 2, Application US/09730174A

Patent No. US50020110871A1

GENERAL INFORMATION: Antibodies and Peptide Antigens for Producing Antibodies having a

TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a

TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Ho

FILE REPERENCE: IMUNE-001A

CURRENT APPLICATION NUMBER: US/09/730,174A

CURRENT FILING DATE: 2000-12-05

NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
(MS-09-730-174A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
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Publication No. US20030175802A1
GENERAL INFORMATIONER:
APPLICANT: Missbichler, Albert
APPLICANT: Schmidt-Gayk, Heinrich
APPLICANT: Noth, Heinz-Jurgen
TITLE OF INVENTION: Method for Determining Parathormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 86.4%; Score 51; DB 9; Best Local Similarity 90.9%; Pred. No. 0.019; Matches 10; Conservative 0; Mismatches
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ORGANISM: Artificial Sequence
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Best Local Similarity 83.3%;
Matches 10; Conservative
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US-09-730-174A-2
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US-09-730-174A-6
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Fatent No. US/2020110871A1

GRNEAL INFORMATION

TITLE OF INVENTION: AARLEAGHES and Peptide Antigens for Producing Antibodies having a
TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid HG

FILE REFERENCE: IMUNE-001A

CURRENT APPLICATION UNBER: US/09/730,174A

CURRENT FILING DATE: 2000-12-05

NUMBER OF SEQ ID NOS: 12
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Patent No. US20020110871A1

GENERAL INFORMATION:

APPLICANT: Zahradnik, R.J.

APPLICANT: Zahradnik, R.J.

TITLE OF INVENTION: Abtlabodies and Peptide Antigens for Producing Antibodies having a TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid HG

FILE REFERENCE: IMUNE-001A

CURRENT APPLICATION NUMBER: US/09/730,174A

CURRENT FILING DATE: 2000-12-05

NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                             FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies US-09-730-174A-1
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Pred. No. 0.0027;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.2%; Score 55; DB 9; I
100.0%; Pred. No. 0.0038;
tive 0; Mismatches 0;
CURRENT APPLICATION NUMBER: US/09/730,174A CURRENT FILING DATE: 2000-12-05 NUMBER OF SEQ ID NOS: 12 SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                  ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
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Best Local Similarity 91.7
Matches 11; Conservative
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Best Local Similarity
Matches 11; Conserv
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US-09-730-174A-1
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US-09-730-174A-4
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LENGTH: 11
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LENGTH: 12
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US-10-168-185-7

Sequence 7, Application US/10168185

Publication No. US20030175802A1

GENERAL INFORMATION:

APPLICANT: Armbruster, Franz Paul

APPLICANT: Armbruster, Albert

APPLICANT: Schmidt-Gayk, Heinrich

APPLICANT: Roth, Heinz-Jurgen

TITLE OF INVENTION: Activity in a Human Sample

FILE REFERENCE: HLZ-004US

CURRENT APPLICATION NUMBER: US/10/168,185

CURRENT FILING DATE: 2002-06-17

PRIOR FILING DATE: 2000-12-18

PRIOR PLING DATE: 2000-12-18

PRIOR PLING DATE: 1999-12-17

NUMBER OF SEQ ID NOS: 11

SOFTHARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-168-185-2
; Sequence 2, Application US/10168185
; Publication No. US2030175802A1
; GENERAL INFORMATION:
APPLICANT: Armbruster, Franz Paul
APPLICANT: Missbichler, Albert
; APPLICANT: Schmidt-Gayk, Heinrich
APPLICANT: Schh, Heinz-Jurgen
; ITLLE OF INVENTION: Method for Determining Parathormone
; TILLE OF INVENTION: Activity in a Human Sample
; FILE REFERENCE: HIZ-004415
; CURRENT APPLICATION NUMBER: US/10/169,185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 76.3%; Score 45; DB 14; Length 9; Best Local Similarity 100.0%; Pred. No. 1.2e+06; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
TITLE OF INVENTION: Activity in a Human Sample FILE REFERENCE: HIZ-00402 CURRENT APPLICATION NUMBER: US/10/168,185 CURRENT FILING DATE: 2002-06-17 PRIOR APPLICATION NUMBER: PCT/EP00/12911 PRIOR APPLICATION NUMBER: DE 19961350 PRIOR APPLICATION NUMBER: DE 19961350 PRIOR PILING DATE: 1999-12-17 NUMBER: OF SEQ ID NOS: 11 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1
1 LENGTH: 10
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83.1%; Score 49; DB

Best Local Similarity 100.0%; Pred. No. 0.0

Matches 10; Conservative 0; Mismatches
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CAGANISM: Homo sapiens
US-10-168-185-7
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US-10-168-185-1
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LENGIH: 9
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US-10-192-673-6
Sequence 6, Application US/10192673
Sequence 6, Application US/10192673
Sequence 6, Application Would Sequence 6, Application No. US20030166838A1
GENERAL INFORMATION:
APPLICANT: Gardella, Thomas J.
APPLICANT: Potts, John T.
APPLICANT: Potts, John T.
APPLICANT: Potts, John T.
APPLICANT: Potts, John T.
TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
TITLE OF INVENTION WIMBER: US/10/192,673
CURRENT APPLICATION WIMBER: US/10/192,673
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Sequence 8, Application US/10168185

Sequence B. Application US/10168185

Publication No. US20030175802A1

GENERAL INFORMATION:

APPLICANT: Armbruster, Franz Paul

APPLICANT: Schmidt-Gayk, Heinrich

APPLICANT: Schmidt-Gayk, Heinrich

APPLICANT: Schmidt-Gayk, Heinrich

APPLICANT: Roth, Heinz-Jurgen

IITLE OF INVENTION: Method for Determining Parathormone

IITLE OF INVENTION: Mothers US/10/168,185

CURRENT FILING DATE: 2002-06-17

PRIOR APPLICATION NUMBER: DE 19961350

PRIOR FILING DATE: 1999-12-17

NUMBER OF SEQ ID NOS: 11

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO
                       Length 9;
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                                                                0; Indels
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100.0%; Pred. No. 1.2e+06;
ative 0; Mismatches 0;
                     72.9%; Score 43; DB 14; 100.0%; Pred. No. 1.2e+06;
                                                                  0; Mismatches
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Ouery Match
Best Local Similarity 100.
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Best Local Similarity 100.
Matches 8; Conservative
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US-10-168-185-8
                                                                                                               1 SVSEIOLMH 9
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CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: PCT/EP00/12911
PRIOR PILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: DE 19961350
PRIOR FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FASTEEQ for Windows Version 4.0
SEQ ID NO 2

TYPE: PRT
, ORGANISM: Homo sapiens
US-10-168-185-2

LENGTH

0

Gaps

. 0

0; Indels

Length 8;

DB 14; L 1.2e+06;

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59.3%; Scc...
100.0%; Pred. No. ...
CURRENT APPLICATION NUMBER: US/10/168,185;
CURRENT FILING DATE: 2002-06-17;
PRIOR APPLICATION NUMBER: PCT/EP00/12911;
PRIOR FILING DATE: 2000-12-18;
PRIOR FILING DATE: 1900-12-18
PRIOR FILING DATE: 1999-12-17;
NUMBER OF SEQ ID NOS: 11
SOFTWARR: FaetSEQ for Windows Version 4.0
SEQ ID NO : 18
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Best Local Similarity 100.
Matches 8; Conservative
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CRGANISM: Homo sapiens
US-10-168-185-3
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US-10-192-673-10
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Sequence 7, Application US/10192673

Publication No. US20030166838A1

GENERAL INFORMATION:

APPLICANT: Gardalla. Thomas J.

APPLICANT: Kronenberg, Henry

APPLICANT: Kronenberg, Henry

APPLICANT: Bridgher, Harald

ITILE OF INVENTION: Bridghyroid Hormone (PTH) and Parathyroid

ITILE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid

ITILE OF INVENTION: Parathyroid Hormone (PTH)

FILE REFREENCE: 0609-4570002.

CURRENT APPLICATION NUMBER: US, 09/421,379

PRIOR PRILING DATE: 1999-10-20

PRIOR FILING DATE: 1999-10-20

PRIOR FILING DATE: 1999-10-22

NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 7

SEQ ID NO 7

SEQ ID NO 7
                                                                                                                                                                                                                        ; OTHER INFORMATION: Description of Artificial Sequence: synthetic; ; OTHER INFORMATION: peptide US-10-192-673-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: peptide
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Publication No. US20030175802A1
GENERAL INFORMATION:
APPLICANT: Armbruster, Franz Paul
APPLICANT: Missbichler, Albert
APPLICANT: Schmidt-Gayk, Heinrich
APPLICANT: Schh, Heinz-Jurgen
ITILE OF INVENTION: Method for Determining Parathormone
           PRIOR FILING DATE: 1999-10-20
PRIOR APPLICATION NUMBER: U.S. 60/105,530
PRIOR FILING DATE: 1998-10-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 9
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77.88;
                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 77.8
Matches 7; Conservative
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1 AVSEIQLLH 9
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Matches 8; Conserv
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US-10-168-185-3
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                                                                               JAPELICANT: Gardella, Thomas J.
APPLICANT: Gardella, Thomas J.
APPLICANT: Gardella, Thomas J.
APPLICANT: Rronenberg, Henry
APPLICANT: Potts, John T.
APPLICANT: Juppner, Harald
TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
TITLE OF INVENTION: Parathyroid Hormone Related Peptide (PTHrP)
FILE REFERENCE: 0609.4570002
CURRENT FILING DATE: 2002-07-11
PRIOR APPLICATION NUMBER: U.S. 09/421,379
PRIOR PILING DATE: 1999-10-20
PRIOR PILING DATE: 1999-10-20
PRIOR PILING DATE: 1998-10-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 10
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: peptide
US-10-192-673-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55.9%; Score 33; DB 14; Length 9; 77.8%; Pred. No. 1.2e+06; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Armbruster, Franz Paul
APPLICANT: Missbichler, Albert
APPLICANT: Schmidt-Gayk, Heinrich
APPLICANT: Roch, Heinrach
APPLICANT: Roch, Heinra-Gurgen
Sequence 10, Application US/10192673 Publication No. US20030166838A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/10168185; Publication No. US20030175802A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 77.8
Matches 7; Conservative
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Page 5
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us-09-/30-1/4a-3.closed.rap
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0; Gaps

Query Match
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels

Search completed: September 5, 2004, 09:49:37 Job time : 33.5 secs

1 SVSEIQL 7

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TITLE OF INVENTION: Activity in a Human Sample FILE REFRENCE: HLZ-004US
CURRENT APPLICATION NUMBER: US/10/168,185
CURRENT FILING DATE: 2002-06-17
PRIOR FILING DATE: 2000-12-18
PRIOR FILING DATE: 1999-12-17
PRIOR FILING DATE: 1999-12-17
PRIOR FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 11
SOFTWARE FRASESQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 7
INVEST FILING DATE: 1999-12-17
SOFTWARE PRASESQ for Windows Version 4.0
INVEST FILING DATE: 1999-12-17
SOFTWARE PRASESQ for Windows Version 4.0
CROANISM: HOMO SADIENS

(0/0/sn) HUD/8 @60d s/4/

us-09-730-174a-4.closed.rpr

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

September 5, 2004, 09:30:43; Search time 9.5 Seconds (without alignments) 121.505 Million cell updates/sec

US-09-730-174A-4 61 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 1 SVSEIQFMHNLG 12 Scoring table: Sequence:

283366 segs, 96191526 residues Searched:

Total number of hits satisfying chosen parameters:

1581

Minimum DB seq length: 0 Maximum DB seq length: 12

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	18	ď.	თ	7	7842		ribosomal protein
4	18	φ.	10	7	6058		sperm-activating p
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o,	16	è.	7	7	I46868		iyosi
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11	16	ė.	10	7	JC1416		hypertrehalosemic
12	16	ů.	10	7	809138		hypertrehalosemic
13	16	26.2	11	7	A32428		amine oxidase (cop
14	15	4.	7	7	\$29735		olyphosphate-
15	15	4.	σ	7	PT0231		Ig heavy chain CDR
16	15	4.	σ	7	A56029	,	N-methylpurine DNA
17	15	4.	10	(7	833844		alpha-2-macroglobu
18	15	4.	10	7	S27873	•	hypothetical prote
19	15	24.6	10	N	S38304		lectin GNL1 alpha
20	15	4.	11	~1	A38841		rhodopsin homolog
21	15	4.	11	N	835490		type II site-speci
22	15	24.6	12	~1	PH1190]] r
23	15	4.	12	N	S51737		
24	14	23.0	4	7	A35779		neuropeptide Antho
25	14	е Н	7	N	85		φ
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27	14	m	89	α	0899		los
28	14	23.0	80	~	49		tic hor
29	14	23.0	œ	~	A44960		neuropeptide Led-C

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ALIGNMENTS

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1 SVSEIQEM 8 8 |:| :||: 1 SISAMQFI Db ò

RESULT 2

carnotin U149 - Carnobacterium sp. (fragment)
C;Species: Carnobacterium sp.
C;Spacession: 458718
R;Stoffels, G.; Nissen-Meyer, J.; Gudmundsdottir, A.; Sletten, K.; Holo, H.; Nes, I.F.
Appl. Environ. Microbiol. S8, 1417-1422, 1992
Aprille: Purification and characterization of a new bacteriocin isolated from a Carnobac A;Reference number: A58718
A;Accession: A58718
A;Accessio

Gaps ő Query Match 29.5%; Score 18; DB 2; Length 7; Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 4; Conservative 0; Mismatches 0; Indels

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3 SEIQ 6 2 SEIQ 5 à g

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T-cell receptor alpha chain V region (Cw3/1F11) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 16-Uul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C;Accession: PH1187
R;Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Width Med. 176, 439-447, 1992
A;Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor.
A;Reference number: S26512; WUID:92364546; PMID:1380061
A37268
Ig heavy chain C region (129) - mouse (fragment)
Ig heavy chain C region (129) - mouse)
C;Decises: Mus musculus (house mouse)
C;Decises: 19-Mar-1997 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998
C;Accession: A37268
B;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A;Title: Heavy and light chain variable region sequences and antibody properties of antiA;Reference number: A38740; MUID:91177923; PMID:1706720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C,Accession: S21205
R;Makiya, R.; Stigbrand, T.
Bur. J. Biochem. 205, 341.345, 1992
A;Title: Placental alkaline phosphatase has a binding site for the human immunoglobulin-
A;Reference number: S21205; MUID:92209522; PMID:1555592
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C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
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44.4%; Pred. No. 3.1e+03;
tive 1; Mismatches 4; Indels
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C;Keywords: heterotetramer; immunoglobulin
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Best Local Similarity 57.1.
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Matches 4; Conservative
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Matches 3; Conservative
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A, Molecule type: mRNA
A, Residues: 1-12 < CAS>
                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-10 <RUF>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sperm-activating peptide (Tyr-2, Asn-3, Gly-5, Ile-9, Asp-10 SAP-1) - slate-pencil urchi C; Species: Heterocentrotus mamillatus
C; Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
C; Accession: A60589
R; Yoshino, K.I.; Kajiura, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguc Comp. Biochem. Physiol. B 94, 739-751, 1989
A; Title: A halogenated amino acid-containing sperm activating peptide and its related ped outs nudus. Echinometra mathaei and Heterocentrotus mammillatus.
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A05169
A05169
A05169
C.Species: Periplaneta americana (American cockroach)
C.Species: Periplaneta americana (American cockroach)
C.Species: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 31-Dec-1993
C.Accession: A05169
R.Mitten, J.L.; Schaffer, M.H.; O'Shea, M.; Cook, J.C.; Hemling, M.E.; Rinehart Jr., I Biochem. Biophys. Res. Commun. 124, 350-358, 1984
A.Ritle: Structures of two cockroach neuropeptides assigned by fast atom bombardment the A.Reference number: A90118; MUID:85046530; PMID:6548628
A.Accession: A05169
A.Accession: Apostory
A.Residues: 1-8 <WIT>
C.Keywords: neuropeptide
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                 ribosomal protein RL41, mitochondrial [validated] - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Bate: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jul-2000
C;Accession: S74420
R;Goldschmidt-Reisin, S.; Graack, H.R.
submitted to the Protein Sequence Database, February 1998
A;Reference number: S78411
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                     A,Molecule type: protein
A,Residues: 1-9 <GGL>
A,Note: the protein is designated as mitochondrial ribosomal protein L41
C,Keywords: mitochondrion, protein biosynthesis; ribosome
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                                                                                                                                                                                                                                                                                                                                                                                             29.5%; Score 18; DB 2; Length 9; 75.0%; Pred. No. 2.8e+05; tive 0; Mismatches 1; Indels
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1; Mismatches

Query Match
Best Local Similarity 42.9%;
Matches 3; Conservative

4 EIQFMHN 10

EVNFSPN 7

29.5%;

Best_Local Similarity 75.0 Matches 3; Conservative

Query Match

:||-YNLG 5

9 HNLG 12

8

A, Accession: A60589 A, Molecule type: protein A, Residues: 1-10 < YOS> C, Superfamily: unassigned animal peptides

3; Conservative

Matches

9 HNLG 12

ò

HRLG 8

Query Match Best Local Similarity

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A;Molecule type: protein

A;Molecule type: protein

B; 2.10 cGAE2>
C;Comment: Hypertrehalosemic factor II lacks the tryptophan modification.
C;Comment: This peptide raises hemolymph levels of trehalose in the cockroach Periplane!
C;Comment: This peptide raises hemolymph levels of trehalose in the cockroach Periplane!
C;Superfamily: adipokinetic hormone and; glycoprotein; hormone, neuropeptide, pyroglutamic ac:
F;Reywords: amidated carboxylic acid (Gln) #status experimental
F;Reinding site: carbohydrate (Trp) (covalent) #status experimental
F;10/Modified site: amidated carboxyl end (Thr) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypertrehalosemic hormone II - stick insect (Extatosoma tiaratum)

A) Alternate names: Can-HrTH-II

C) Species: Extatosoma tiaratum

C) Species: Extatosoma tiaratum

C) Date: 30-Jun-1992 #sequence_revision 24-Oct-1997 #text_change 31-Oct-1997

C) Accession: 80138

R) Accession: 80138

R) Gaede, G; Rinehart, K.L.

Biol. Chem. Hoppe-Seyler 371, 345-354, 1990

A) Fittle: Primary structures of hypertrehalosaemic neuropeptides isolated from the corporentalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombarx

A) Reference number: 808995; MUID:90253659; PMID:2340112
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A,Molecule type: protein
A,Roseidues: 1-10 cGAE>
A,Roseidues: 1-10 cGAE>
A,Roseidues: 1-10 cGAE>
A,Roseidues: amino-terminal residue forms pyrrolidone carboxylic acid; therefore, C,Superfamily: adipokinetic hormone
C,Superfamily: adipokinetic hormone
C,Reywords: amidated carboxyl and hormone; neuropeptide; pyroglutamic acid
F,1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F,10/Modified site: amidated carboxyl end (Thr) #status experimental
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Cispecies: Sus scrofa domestica (domestic pig)
Cispecies: Sus scrofa domestica (domestic pig)
Cispecies: 12-oct.1989 #sequence_revision 31-Dec-1993 #text_change 06-Sep-1996
Cidacession: A32428
Rivan der Weer, R.A.; van Wassenaar, P.D.; van Brouwershaven, J.H.; Duine, J. Bliochem. Biophys. Resc. Commun. 159, 726-733, 1989
Biochem. Biophys. Resc. Commun. 159, 726-733, 1989
A;Title: Primary structure of a pyrrologuinoline quinone (PQQ) containing pea A;Title: Primary structure of a pyrrologuinoline quinolective: Drotein
A;Reference number: A32428; MUID:89193662; PMID:2539124
A;Accession: A32428; MUID:89193662; PMID:2539124
A;Residues: 1-7, K', 9-11 < VAN>
A;Nolecule type: protein
A;Residues: 1-7, K', 9-11 < VAN>
A;Note: the modified residue thought by the authors to be pyrrologuinoline qC;Reywords: oxidoreductase; quinopprotein; topaquinone
C;Reywords: oxidoreductase; quinopprotein; topaquinone
C;Reywords: oxidoreductase; quinopprotein; topaquinone
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NyAlternate names: neuropeptide Cam-HrTH-I
NyContains: hypertrehalosemic factor II
C;Species: Carausius morcsus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: UC148; S07157
R;Gaede, G; Kellner, R; Rinehart, K.L.; Proefke, M.L.
Biochem. Biophys. Res. Commun. 189, 1303-1309, 1992
A;Title: A tryptcphan-substituted member of the AKH/RPCH family isolated from a stick in A;Reference number: UC1416; MUID:93129188; PMID:1482345
A;Accession: UC1416
A;Accession: UC1416
A;Residues: 1-10 GAE1>
R;Gaede, G; Rinehart Ur., K.L.
Biol. Chem. Hoppe-Seyler 368, 67-75, 1987
A;Title: Primary structure of the hypertrehalosaemic factor II from the corpus cardiacum A;Reference number: S07157; MUID:87157103; PMID:3828078
A;Accession: S07157
                                                                                                                                                                                                                                                                                                                                                        rabbit alpha- and beta-ventricula
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C;Species: unidentified bacterium
C;Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 10-Jul-1998
C;Accession: G58502
R;Binette, J.P.; Binette, M.B.
Submitted to the Protein Sequence Database, October 1996
A;Description: The proteins of kidney and gallbladder stones.
A;Reference number: A58501
A;Reference number: A58501
A;Residues: 1-9 protein
A;Residues: 1-9 cally
A;Molecule type: protein
A;Residues: 1-9 cally
A;Rocte: a secondary sequence AaKENPXD was also found
                                                                                                                               alpha-myosin heavy chain - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 05-Nov-1999
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R.;Friedman, D.J.; Umeda, P.K.; Sinha, A.M.; Hsu, H.
Proc. Natl. Acad. Sci. U.S.A. 81, 3044-3048, 1984
A.Title: Characterization of genomic clones specifying rabbit alpha- and A. Reference number: 146868; MUID:84221901; PMID:6328491
A. Accession: 146868
A. Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Resiques: 1-7 <FRI>A.Resiques: 1-7 <FRI
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4; Mismatches 1
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Delybhosphate-glucose phosphotransferase (BC 2.7.1.63) - Propionibacterium freudenreichi (Species: Propionibacterium freudenreichi subsp. shermanii (Spacies: Propionibacterium freudenreichii subsp. shermanii (Spate: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 03-Jun-2002 (Spate: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 03-Jun-2002 (Spate: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 03-Jun-2002 (Spate: 19-Mar-1997 #text_change 03
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RESULT 15 PT0231

Deavy chain CDR3 region (clone 1-118B) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0231
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and A;Reference number: PT0222; MUID:91108337; PMID:1899102

A Accession: PT0231
A;Molecule type: DNA
A;Residues: 1-9 < YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

0; Gaps Query Match 24.6%; Score 15; DB 2; Length 9; Best Local Similarity 33.3%; Pred. No. 2.8e+05; Matches 2; Conservative 2; Mismatches 2; Indels

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7 FMHNLG 12

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: |: | 1 YTHSSG 6

Search completed: September 5, 2004, 09:37:44 Job time : 10.5 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

September 5, 2004, 09:27:07; Search time 6.5 Seconds (without alignments) 96.130 Million cell updates/sec Run on:

US-09-730-174A-4 61 1 SVSEIQFMHNLG 12 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched:

501 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 12

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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(C TISSUB—CORPORA cardiaca;
(C X MEDLINE=89145002; PubMed=3226948;
(A MEDLINE=89145002; PubMed=3226948;
(A Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;
(A Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;
(A TSQUENCE analyses of two neuropeptides of the AKH/RPCH-family from RT the lubber grasshopper. Romalea microptera.";
(C T = PUNCTYON: Hypertrehalosaemic factors are neuropeptides that C C major carbohydrate in the hemolymph of insects).
(C = Levate the level of trehalose in the hemolymph (trehalose is the C C major carbohydrate in the hemolymph of insects).
(C = SUBCENLIUAR LOCATION: Secreted.
(C = SIMILARITY: Belongs to the AKH / HRTH / RFCH family.
(C = SIMILARITY: Belongs to the AKH / HRTH / RFCH family.
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(C = SIMILARITY: Belongs to the AKH / HRTH / RFCH family.
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(C = SIMILARITY: Belongs to the AKH / HRTH / RFCH / MFCH / MF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92321768; PubMed=1622206;
Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Purification and characterization of a new bacteriocin isolated from a Carnobacterium sp.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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01-FBE-1994 (Rel. 28, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
RO I (Hypertrehalosaemic factor).
Romalea microptera (Lubber grasshopper).
Romalea microptera (Lubber grasshopper).
Romalea Microptera (Lubber grasshopper).
Neoptera, Orthoptera (Crthoptera), Orthoptera, Acridomorpha, Acridoidea, Romalea.
                                                                                                                                                                                                                                                                                                                      Carnobacterium sp. (strain U149).
Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29.5%; Score 18; DB 1; Length 10; ilarity 33.3%; Pred. No. 1.1e+03; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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056236745771A9C4 CRC64;
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SEQUENCE 7 AA; 786 MW; 741776D05B05B810 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29.5%; Score 18; DB 1; Le
100.0%; Pred. No. 1.4e+05;
tive 0; Mismatches 0;
                                                                                                                                                                      01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Lantibiotic carnocin UT49 (Fragment).
                                                                                                      7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                      STANDARD;
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nes 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=35782;
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                                                                                                                                                                                                                                                                                                                                                                                                  Carnobacterium
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HTF1_ROWNI

DF1_ROWNI

DF2_01_NOV-1990

DT 01-PEB-1994

DE RO 1 (Hypert

OC Bukaryota, M

OC Acridoides, OC

Neoptera, OC

OC Acridoides, OC

OC Acridoides, OC

NEDINE-8914

RA Gaede G., Hi

RT NEDINE-8914

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CC -!- SURCELLU

DR NEOSITE; PSO

KW Neuropeptide

FT MOD_RES

FT MOD_RES
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AD 01-4UN-1
DT 01-4UN-1
DT 16-OCT-2
DE LANTIDIG
OC BACTERIO
OC CARNODAG
OC CARNODAG
OC CARNODAG
OC RESULDE
RA SEQUENCE
RA NES 1.F
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Gaps

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Best Loca Matches

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Gaede G., Rinehart K.L. Jr., "Primary structures of hypertrehalosaemic neuropeptides isolated from the corpora cardiaca of the cockroaches Leucophea maderae, Gromphadorhina portentosa, Blattella germanica and Blatta orientalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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01-701-1998 (Rel. 11, Created)
01-701-1994 (Rel. 28, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Hypertrehalosaemic factor II (HTF-II) (HYRTH-II) (Hypertrehalosaemic
                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-98054539; PubMed-9392829;
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D., Davey M., East P.D., Thorpe A.;
"Lepidopteran peptides of the allatostatin superfamily.";
Peptides 18:1301-1309(1997).
-!- SIMILARITY: Belongs to the allatostatin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neoptera, Orthopteroidea, Phasmatodea, Euphasmida, Phasmatoidea, Heteronemiidae, Carausius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES=C.morosus; TISSUB=Corpora cardiaca;

MEDLINE=8715-7103; PubMed=3928079;

Gaede G., Rinehart K.L. dr.;

"Primary structure of the hypertrehalosaemic factor II from the

corpus cardiacum of the Indian stick insect, Carausius morosus,

determined by fast atom bombardment mass spectrometry.";

Biol. Chem. Hoppe-Seyler 368:67-75(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                         Cydia pomonella (Codling moth).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Lepidoptera, Glossata, Ditrysia,
Tortricoidea, Tortricidae, Olethreutinae, Cydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neuropeptide II).
Carausius morosus (Indian stick insect), and
Extatosoma tiaratum (Stick insect).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 16; DB 1; Lengtn e, Pred. No. 1.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 AA; 936 MW; 0B2879C45B573767 CRC64;
                                                                                                                                      30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES=E.tiaratum; TISSUE=Corpora cardiaca; MEDLINE=90253659; PubMed=2340112;
                                                                                                      8 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Conservative
                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neuropeptide; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
1 QVNFTPNWG 9
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Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 MHNLG 12
                                                                                                                                                                                                                                                                                                           NCBI_TaxID=82600;
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                                                                                                                                                                                                          Cydiastatin 6
                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Larva;
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B AA.

STANDARD;

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15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 36, Last sequence update)
Allergen Fus s I3596* (Fragment).
Fusarium solani (subsp. pisi) (Nectria haematococca).
Fusaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
                                                                                                                                                                                                                                                                                                                                         Query Match 24.6%; Score 15; DB 1; Length 8; Best Local Similarity 66.7%; Pred. No. 1.40+05; Matches 2; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                             STRAIN=IARI 3596; TISSUE=Mycelium;
Verma J., Gangal S.V.;
Submitted (JUL)
-!- ALLERGEN: Causes an allergic reaction in human.
                                                                                                                                                                                                                                                                                              8 AA; 898 MW; C372C441F5B69041 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                             9 HNL 11
               FUSSO
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SEQUENCE
                                                                                                                                                                                                                                                                              Allergen.
                                                                                                                                                                                               SEQUENCE
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0
                                                                       SPECIES—C.mocrosus; TISSUB=Corpora cardiaca;

MEDLINE=93129188; PubMed=1482345;

Gaede G., Kellner R., Khaner K., Ur., Proefike M.L.;

Gaede G., Kellner R., Khaner C., Ur., Proefike M.L.;

The strick insect corpus cardiacum.";

E sochem: Bloghys. Res. Commun. 189:1303-1309(1992).

E sochem: Bloghys. Res. Commun. 189:1303-1309(1992).

I slocker: Bloghys. Res. Commun. 189:1303-1309(1992).

I FUNCTION: Hypertrehalosaemic factors are neuropeptides that elevate the level of trehalose in the hemolymph (trehalose is the major carbohydrate in the hemolymph of insects).

I SUBCELULAR LOCATION: Sected.

I MASS SPECTROMETRY: WW=1308.61; METHOD=FAB.

I SIMILARITY: Belongs to the AKH / HRTH / RPCH family.

PIR: 509138; 509138.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                          PIR; S09138; SUJJJJ, KH.
INCEPPRO, IPRODO247; AKH.
INCEPPRO, IPRODO247; AKH.
NEUSTEP, PS00256; AKH; 1.
Neuropeptide; Amidation; Glycoprotein; Pyrrolidone carboxylic acid.
NOD RES

CARBOHYD

MOD_RES

NOD_RES

NOD_RES

NOD_RES

NOD_RES

NOD_RES

NOD_RES

NAN: 9B9036745771A9D1 CRC64;
and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment mass spectrometry. ", \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUB-Skin secretion; Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.; "Peptides from the skin glands of the Australian buzzing tree frog Litori electrica. Comparison with the skin peptides from Litoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Litoria rubella (Desert tree frog).

Litoria rubella (Desert tree frog).

Aukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea;

Pelodryadinaa; Litoria.
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Pred. No. 2.7e+03;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.6%; Score 15; DB 1; Length 5; 66.7%; Pred. No. 1.4e+05; 1ive 1; Mismatches 0; Indels
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SEQUENCE 5 AA, 630 MW, 668761F2C9A00000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 AA.
                               Biol. Chem. Hoppe-Seyler 371:345-354(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aust. J. Chem. 52:639-645(1999).
-- SUBCELLULAR LOCATION: Secreted.
-- TISSUB SPECIFICITY: Skin.
Amphibian defense peptide; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 33.3%;
Matches 3; Conservative
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Best Local Similarity
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1 FVH 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rubella.";
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Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
10-GCT-2003 (Rel. 42, Last annotation update)
RNA polymerase beta subunit (EC 2.7.7.48) (Large structural protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PERMINE STATES AND STA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Belongs to the paramyxoviruses L protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses, ssRNA negative strand viruses, Mononegavirales,
Paramyxoviridae, Paramyxovirinae, Morbillivirus.
NCBI_TaxID=11240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 AA; 1105 MW; 9C2B7FD452D5A2D5 CRC64;
                                                                                                                                                                                                                      10 AA.
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Transferase; RNA-directed RNA polymerase.
NON TER
SEQÜENCE 10 AA; 1105 MW; 9C2B7FD452D5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phocine distemper virus (PDV).
                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [L protein) (Fragment).
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SEQUENCE FROM N.A.
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5 HNV 7
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P35946;
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RESULT 7

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                                                                                                                                                                                                                                                                             Flengsrud R., Skjeldal L.;
"Two-dimensional gel electrophoresis separation and N-terminal
"Two-dimensional gel electrophoresis from Clostridium pasteurianum W5.";
sequence analysis of proteins from Clostridium pasteurianum W5.";
Electrophoresis 19:802-806 (1998).
-!- FUNCTION: This protein promotes the GTP-dependent translocation of the nascent protein chain from the A-site to the P-site of the
                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
EF-G/FE-2 subfamily.
INTERPO.; IPRO00795; EF GTPbind.
PROSITE; PS00301; EFACTOR GTP; PARTIAL.
Elongation factor; Protein biosynthesis; GTP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Heart;
MEDLINE=98163340; PubMed=9504812;
Dunn M.J., Corbett J.M., Wheeler C.H.;
"HSC-2DPAGE and the two-dimensional gel electrophoresis database of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Canis familiaris (Dog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria, Carnivora, Fissipedia, Canidae; Canis.
                                                                                                                                                                                 Clostridium pasteurianum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
NCBI_TaxID=1501;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-1996 (Rel. 34, Created)
15-UL-1998 (Rel. 36, Last sequence update)
16-UL-1998 (Rel. 42, Last annotation update)
NADH-ubiquinnon oxidoreductase 24 kba subunit (EC 1.6.5.3)
(EC 1.6.99.3) (Fragment).
Score 15; DB 1; Length 10;
Pred. No. 4.3e+03;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 15; DB 1; Length 11;
Pred. No. 4.7e+03;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               11 AA; 1337 MW; 412E71F1D9C33B17 CRC64;
                                                                                                                                                  Last sequence update)
Last annotation update)
EF-G) (CP 5) (Fragment).
                                                                                                                   11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 AA.
                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dog heart proteins.";
Electrophoresis 18:2795-2802(1997).
                                                                                                                                                                                                                                                                    MEDLINE=98291870; PubMed=9629918;
                                                                                                                                  15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last seque
28-FEB-2003 (Rel. 41, Last anno
Elongation factor G (EF-G) (CP
  24.6%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.6%;
25.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Cuery Match
Best Local Similarity 25.v...
                       3; Conservative
                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 IQFMHNLG 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 LEKFONIG 11
            Local Similarity
                                           1 SVSEI 5
                                                               6 IONAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUHM CANFA
P49820;
                                                                                                                 EFG CLOPA
P81350;
                                                                                                                                                                                                                                                          STRAIN=W5
                                                                                                                                                                                                                                                                                                                                                                                                                       NON TER
SEQUENCE
  Query Match
                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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             Best Loca
Matches
                                                                                              RESULT 9
EFG_CLOPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
                                                                                                                             -:- Fraction of the Bold of the Uniquinone = NAD(+) + ubiquinol.
-:- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + reduced acceptor.
-:- COFACTOR Binds 1 2Fe-28 cluster (Potential) + reduced acceptor.
-:- COFACTOR: Binds 1 2Fe-28 cluster (Potential) + reduced acceptor.
-:- SUBUNIT: Mammalian complex is composed of 45 different subunits.
-:- SUBCELLULAR LOCATION: Matrix and cytoplasmic side of the mitochondrial inner membrane.
-:- SIMILARITY: Belongs to the complex I 24 kDa subunit family.
HSC-2DPAGE; P49820; DGG.
INTER-PRO; IPRO20223; COMPLEXI 24kDa.
PROSITE; P801099; COMPLEXI 24kDa.
PROSITE; P801099; COMPLEXI 24k; PARTIAL.
Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Metal-binding;
                                         BELIEVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=ATCC 13315;
MEDLINE=93087186; PubMed=1454536;
Smith M.D., Longo M., Gerard G.F., Chatterjee D.K.;
"Cloning and characterization of genes for the Pvul restriction and modification system.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLEANES AFTER T-4.
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give
specific double-stranded fragments with terminal 5'-phosphates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Proteus:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Endonuclease PvuI)
FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELL TO BE UBIQUINONE. COMPONENT OF THE FLAVOPROTEIN-SULFUR (FP) FRAGMENT OF THE BNZYME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 20:5743-5747(1992).
-!- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE CGATCG AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Restriction system; Hydrolase; Nuclease, Endonuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        267F5369C9C72DD8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 AA; 1300 MW; 9F0CDE7955B72B1A CRC64;
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60.0%; Pred. No. 4.7e+03;
tive 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 15; DB 1; I
Pred. No. 4.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-001-1993 (Rel. 26, Created)
01-001-2003 (Rel. 26, Last sequence update)
10-007-2003 (Rel. 42, Last annotation update)
Type II restriction enzyme Pvul (EC 3.1.21.4)
(R.Pvul) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 24.6%; Score 15; DB Best Local Similarity 66.7%; Pred. No. 4.7e Matches 2; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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PIR, S35490; S35490.
REBASE; 1541; PvuI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 AA; 1099 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Iron-sulfur; Iron; 2Fe-2Š.
NON TER 11 11
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Best Local Similarity 60.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proteus vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=585;
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SEQUENCE
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Gaps

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1; Indels

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Mismatches
                                                                                                                                                                                                                                            PRT;
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Litoria rubella (Desert tree frog)
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7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 33.3%;
Matches 2; Conservative 2
2; Conservative
                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI TaxID=104895;
                                                   MHNLG 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :|:
QIPWFH 6
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                                                                                   2 MYDFG
                                                                                                                                                                                                                                         LITRU
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P81821;
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                                                   ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                    TYS1 LITRU

AC 28-F2BS

DT 28-F2BS

DT 28-F2BS

DT 18-F2BS

DT 18-F2BS

OC Bulkary

OC Bulkary

OC Bulkary

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RN III III

RR T III III

RR AMBLI

CC - I - F

CC - I - C

CC - C

CC - I - C
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE, AND MASS SPECTROMETRY.
MEDLINE=9319122; PubMed=1973541;
Grimmelikhuijzen C.J.F., Rinehart K.L. Jr., Jacob E., Graff D.,
Reinscheid R.K., Nothacker H.-P., Staley A.L.,
"Isolation of L-3-phenyllacty1-Leu-Arg-Asn-NH2 (Antho-RNamide), a sea aneone neuropeptide containing an unusual amino-terminal blocking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
ALL7 CYDPO
ID ALL7 CYDPO
OSTANDARD; PRT; 7 AA.
AC P82158;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
C Cydiastatin 7.
C Cydia pomonella (Codling moth).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE.
TISSUE-Larva;
TISSUE-Larva;
TISSUE-Larva;

MIDLINE-98054539; PubMed=9392829;

Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D., Davey M., East P.D., Thorpe A.;

"Lepidopteran peptides of the allatostatin superfamily.";

Peptides 18:1301-1309(1997).

-: SIMILARITY: Belongs to the allatostatin family.
                                                                                                                                                                                                                                                                                                                                                               Anthopleura elegantissima (Sea anemone).
Bukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
Nynantheae; Actiniidae; Anthopleura.
NCBI_TaxID=6110;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23.0%; Score 14; DB 1; Length 4; 50.0%; Pred. No. 1.40+05; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23.0%; Score 14; DB 1; Length 7; 40.0%; Pred. No. 1.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 4 A A AMIDATION.
4 AA; 549 MW; 64540729A0000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 7 AA; 873 MW; 672879CABB569350 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  group.";

Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414(1990)
-1- SUBCELLULAR LOCATION: Secreted.
-1- ILSSUE SPECIFICITY: Neuron specific.
-1- TISSUE SPECIFICITY: MW=549.3; METHOD=FAB.
PIR; A35779; A35779.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L-3-PHENYLLACTYL.
                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 50.00,
Best Local Si Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neuropeptide; Amidation.
MOD_RES 1 1
MOD_RES 4 4
SEQUENCE 4 AA; 549 MW.
                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                 1 SVSEI 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 FMHN 10
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                                                 || |:
SVDEL
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                                                                                                                                                                                                    FLRN ANTEL
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SEQŪENCE
                                                                                                                                                                               FLRN_ANTEL
                                                                                                                                          RESULT 12
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Gaps
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Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
Pelodryadinae; Litoria.
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-i- FUNCTION: May act as a neurotransmitter or neuromodulator.
-i- SIMILARITY: Bellongs to the allatostatin family.
Neuropeptide; Amidation; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Cerebral ganglion, and Thoracic ganglion;
MEDLINE=99121193; PubMed-9461295;
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
Thorpe A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carcinus maenas (Common shore crab) (Green crab).

Carcinus maenas (Common shore crab) (Green crab).

Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;

Eubrachyura; Portunoidea; Portunidae; Carcinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 14; DB 1; Length 7; Pred. No. 1.48+05; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 AA; 983 MW; 7401E9D3676046B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAX-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 AA.
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ALLS CARMA
DT ALLS CARMA
DT 30-MAY
RN CARCING
RN CARCING
RN TISSUE
RN THOUSE
RN THOUS
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 MOD_RES
 8
 8 AMIDATION (POTENTIAL)

 SEQÜENCE
 8 AA;
 919 Mw;
 C82879D5AB569AB5 CRC64;

0; Gaps Query Match 23.0%; Score 14; DB 1; Length 8; Best Local Similarity 40.0%; Pred. No. 1.4e+05; Matches 2; Conservative 2; Mismatches 1; Indels

; 0

8 MHNLG 12 |::| 3 MYSFG 7

ò qq Search completed: September 5, 2004, 09:35:03 Job time: 7.5 secs

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GenCore version 5.1.6
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using sw model
OM protein - protein search, using sw model

September 5, 2004, 09:30:03; Search time 27.5 Seconds (without alignments) 137.681 Million cell updates/sec Run on:

US-09-730-174A-4 61 1 SVSEIQFMHNLG 12 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1017041 segs, 315518202 residues Searched:

2565 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 12

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL_25:* Database :

sp_bacteria:*
sp_bacteria:*
sp_human:*
sp_invertebrate:*
sp_invertebrate:*
sp_mammal:*
sp_organelle:*
sp_organelle:*
sp_bhage:*
sp_bhage:*
sp_bhage:*
sp_trebrate:*
sp_vertebrate:*
sp_pacteriap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

3 limnodyna aeromonas aeromonas borrelia b	V44UU acromonas e Q9fx10 1111um long Q9d68 elaeis guin P8233 6 pisam sativ P82085 limnodynast	٠ ٢ ٦ ٣ ه ٠	- 00 g 8 V	Ogur95 pichia angu Q9c057 homo sapien Q9bdc8 pongo pygma Q9bdq9 gorilla gor Q9bdq0 pan rroglod Q9bdc9 pan paniscu Q9unv5 homo sapien Q91u19 influenza a
9 2 Q4437 9 2 Q44468 9 2 Q4468 9 2 Q8KU3 9 2 Q4328	10 10 13	8 4 Q15894 8 8 Q34909 8 13 Q90493 9 2 Q43960	10201	11 3 09UR95 11 6 09CC5 11 6 09EDC8 11 6 09EDD0 11 6 09EDD0 11 6 09EDC9 12 4 09UNV5 7 8 12 091UR5 8 12 091UR5
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ALIGNMENTS

RES	RESULT 1			
in	Q9PS71	PRELIMINARY;	PRT;	11 AA.
AC	Q9PS71;			
DŢ	01-MAY-2000	(TrEMBLrel. 13,	Created)	
Τα	01-MAY-2000	(TrEMBLrel. 13,		Last sequence update)
ΤQ	01-JUN-2002	(TrEMBLrel. 21,		Last annotation update)
DE	Fibrinolytic	metalloproteina		ent).
SO	Agkistrodon	Agkistrodon contortrix.	1	
00	Eukaryota;	Metazoa; Chordata	Craniat	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
ပ္ပ	Lepidosauri	a; Squamata; Scle	rodlossa;	Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Ö	Viperidae;	Viperidae, Crotalinae, Ackistrodon.	trodon.	
ŏ	NCBI TaxID=8720;	8720;		
RN	i E	•		
RP	SEQUENCE			
RX	MEDLINE=913	MEDLINE=91378546; PubMed=1898066;	8066;	
RA	Guan A.L.,	Retzios A.D., Hen	derson G.1	N., Markland F.S.Jr.;
RT	"Purificati	on and characteri	zation of	"Purification and characterization of a fibrinolytic enzyme from ve
RT	of the sout	hern copperhead s	nake (Aqk:	of the southern copperhead snake (Adkistrodon contortrix
RT	contortrix).";		1	
RL	Arch. Bloch	Biophys.	289:197-207(1991),	991),
F	NON TER			
S	ш	A;	7CA02D1D	7CA02D1D41E8772B CRC64;
Ó	Ouery Match	39.3%	Score 24:	. DB 13: Length 11:
ďΣ	Best Local Sim	Similarity 100.0%;	-	. 5.9e+02
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Created) Last sequence update) 8 AA. Q9TT78 PRELIMINARY; Q9TT78; 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13,

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Paramyxoviridae, Paramyxovirinae, Morbillivirus.
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Best Local Similarity 60...
3, Conservative
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nes 3; Conservative
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             NCBI_TaxID=11232;
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STRAIN-DOG #5526/89;
Idermann H., Harder T., Haas L.;
Genetic analysis of the central untranslated genome region and the proximal coding part of the F gene of wild-type and vaccine distemper morbility
                                                                                                                                                                                                                          Gaps
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                                                                                      SEQUENCE FROM N.A. MEDLINE=21015404; PubMed=11130975; MEDLINE=21015404; PubMed=11130975; Brouillette J.A., Andrew J.R., Venta P.J.; Brouillette J.A., Andrew J.R., Venta P.J.; metilectide diversity in dogs with a pool-and-sequence method.";
                                             Euteleostomi;
Canis.
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Viruses; ssRNA negative-strand viruses; Mononegavirales;
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                                                                                                                                                                                                                                                                                                                                                                                                      Viruses, ssRNA negative-strand viruses, Mononegavirales, Paramyxoviridae; Paramyxovirinae, Morbillivirus.
                                   Canis familiaris (Dog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae,
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Last annotation update)
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Last annotation update)
   01-DEC-2001 (TYEMBLrel. 19, Last annotation updaté)
Thymidylate synthase (Fragment).
                                                                                                                                                                                 8 AA; 899 MW; 6731A1E059CAA867 CRC64;
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                                                                                                                                        Mamm. Genome 11:1079-1086(2000).
EMBL; AF202073; AAF20918.1; -.
NON_TER 1
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01-NOV-1998 (TrEMBLrel. 08,
01-NOV-1998 (TrEMBLrel. 08,
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nes 3; Conservative
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SEQUENCE
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Annra; Neobatrachia; Bufonoidea; Myobatrachidae;
Limnodynastinae; Limnodynastes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

STRAIN=Dog #10757/96;

Liermann H., Harder T., Haas L.;

Liermann H., Harder T., Has L.;

Liermann H., Harder T., Has L.;

Liermann H., Harder T., Has L.;

Jenetic analysis of the central untranslated genome region and the proximal coding part of the F gene of wild-type and vaccine distemper morbilliviruses.";

Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.

NON_TER PAPOZ6234; AAC09164.1;

NON_TER PAPOZEZ34; AAC09164.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Eukaryota, Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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Pred. No. 1e+06;
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Obermaier B., Piravandi E., Rinke M.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAY-2000 (TrEMBLrel. 13, Last annotation update)
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Last annotation update)
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100.0%; Pred. No. ...
'... 0; Mismatches
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01-NOV-1999 (TrEMBLrel. 12, Last seq
01-OCT-2002 (TrEMBLrel. 22, Last ann
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Gaps

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Indels

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Q15342 Q15342;

RESULT 7

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SEQUENCE FROM N.A.

MEDLINE=8503320; PubMed=6092695;

SULTANE-P., Jansen H.W., Bister. Kapp U.R.,;

SULTAN I region of avian carcinoma virus MH2 shares sequence elements with avian sarcoma viruses Y73 and SR-A.",

J. Virol. 52:703-705(1994).

EMBL; K03100; AAA42388.1; -.

NON TER. 1
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                                                                                                        Length 12,
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llarity 28.6%; Pred. No. 1.5e+04;
Conservative 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MH2, proviral DNA, myc to 3' LTR (Fragment).
Avian carchnoma virus.
Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=82260445; PubMed=6286214; MEDLINE=82260445; PubMed=6286214; MCKeoun M., Firtel R.A.; Morton multigene family of Dictyostelium."; Cold Spring Harb. Symp. Quant. Biol. 46:495-505(1982). EMBL; K02956; AAA33150.1; DINED. SEQUENCE 11 AA; 1205 MW; 728B4C14C6C2CAAB CRC64;
                                                                  9A5E59B65452C9CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE 12 AA; 1466 MW; 72E4B884F30736DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
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Pred. No. 1.1e+04;
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Q85631;
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Q23876
ID Q23876
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MEDLINE=96226397; PubMed=8634147;

MEDLINE=96226397; PubMed=8634147;

Alovanon D., Bernstein Y., Negreau V., Ghozi M.C., Bar-Am I.,

Aloya R., Goldenberg D., Loveem J., Groner Y.;

Alarge variety of alternatively spliced and differentially expressed

"A large variety of alternatively spliced and differentially expressed

"RA Large variety of alternatively spliced and differentially expressed

"NA Cell Biol. 15:75-185 (1996).

BMAL, X90978; CAA62465.1;

NON TER

SEQÜENCE 10 AA, 1254 MW; 8D99287B441AF365 CRC64;
                                                                                                                                                                                   Gaps
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Chloroplast.
Ebukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Malvales; Malvaceae; Malvoideae; Anoda.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D., "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using chloroplast DNA sequences of ndhr and the rplif intron."; Syst. Bot. 27.333-350(2002).
EMBL, AF384567; AAMS0405.11, -.
GO, GO:0009507; C:chloroplast; IEA.
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Pred. No. 8.8e+03;
2; Mismatches 3; Indels
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                                                                                                                                      Query Match

29.5%; Score 18; DB 3; Length 8;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 1; Indels
                                      Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
EMBL, Z71612; CAA96271.2; -.
                                                                                                  5CA441E449C9C720 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2002 (TrEMBLrel. 22, Created)
1-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0TN-2003 (TrEMBLrel. 24, Last annotation update)
Ribosomal protein 16 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                   10 AA
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                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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                                                                             NON TER 1 1 SEQUENCE 8 AA; 1005 MW;
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Best Local Similarity 44.4.
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A. STRAIN=FY1679;
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TISSUE=Blood;
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2 IHNV 5
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RESULT 13
Q8JJ20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAINSTOCK 172;
MIDLINES #505521;
MIDLINES #505521;
Pritchard A.E., Seilhamer J.J., Cummings D.J.;
Pritchard A.E., Seilhamer J.J., Cummings D.J.;
Pramecium mitochondrial DNA sequences and RNA transcripts for cytochrome oxidase subunit I, URFI, and three ORFs adjacent to the replication oxigin.";
Gene 44:243-253 (1986).
ENBL; M15280; AAA79267.1;
GO: GO:0005739; C:mitochondrion; IEA.
Mitochondrion.
NON_TER
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UNOV-2003 (TrEMBLrel. 24, Last annotation update)
Alpha-myosin heavy chain (Fragment).
Oryctolagus cuniculus (Rabbit).
Bukaryota, Matazoa; Chordata, Craniata, Vertebrata; Euteleostomi; Mammalia; Butheria: Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                  Mitochondrion.
Bukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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Friedman D.J., Umeda P.K., Sinha A.M., Hsu H.-J., Jokovcic S.,
Rabinowitz M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 17; DB 8; Length 11;
Pred. No. 1.5e+04;
3; Mismatches 0; Indels
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11 AA; 1266 MW; 1D84259D16D046D4 CRC64;
                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 81:3044-3048(1984).
EMBL; K01688; AAA31415.1; -.
PIR; I46868; I46868.
NON TEST OF TARY OF TAR
                                                                                                                                11 AA
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Best Local Similarity 50...
3; Conservative
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                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                           Paramecium tetraurelia.
                                                                                                                                                                                                                                                                                       Pl protein (Fragment)
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Best Local Similarity
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|SLNQIQ 7
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                                                              RESULT 11
Q35374
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1028742
AC 028744
AC 02874
DT 01-NO
DT 01-NO
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                                                                                                                                                                Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Archosauria, Aves, Neognathae, Galliformes, Phasianidae; Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zumstein E., Pearson B.M., Kalogeropoulos A., Schweizer M.;
"A 29.425 kb segment on the left arm of yeast chromosome XV contains more than twice as many unknown as known open reading frames.";
Yeast 11:975-986(1995).
Benbl; X83121; CAA58183.1; -. /
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Saccharomycetales, Saccharomycetaceae, Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ·,
                                                                                                                                                                                                                                                                                                                                                Wang Q., Li N., Li H.;
"Cloning and sequencing of 3' UTR of EXFABP gene in chicken.";
"Cloning and sequencing of 3' UTR of EXFABP gene in chicken.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AR487519; AAL96665.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26.2%; Score 16; DB 13; Length 7; 60.0%; Pred. No. 1e+06; 1; Indels iive 1; Mismatches 1; Indels
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Last annotation update)
                    Q8JJ20,
01-CCT-2002 (TrEMBLrel. 22, Created)
01-CCT-2002 (TrEMBLrel. 22, Last sequence update)
01-CCT-2002 (TrEMBLrel. 22, Last annotation update)
Extracellular fatty acid binding protein (Fragment)
EXFABP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DNA CORF'S from chromosome XV (Fragment).
Sacoharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 AA; 879 MW; 7B5322D2C441E058 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 AA; 780 MW; 72CB1AB2D5BEBB70 CRC64;
7 A.A.
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(TrEMBLrel. 01, I
(TrEMBLrel. 22, I
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Best Local Similarity 60...
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PRELIMINARY;
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040659;
01-NOV-1996 (
01-NOV-1996 (
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Q40659
ID Q40653
AC Q40653
DT 01-NO
DT 01-OC
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DE Alpha-amylase (Fragment).

OS Oryza sativar (Rice).

OC Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Ehrhartoideae; Oryzeae; Oryza.

OX NCB1 TaxID=4530;

RN [1] TaxID=4530;

RN [2] TaxID=450;

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Search completed: September 5, 2004, 09:37:00 Job time : 28.5 secs

5 IQFWHNL 11 :| ::|: 1 MQVLNNM 7

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(0/0/sn) 40/0/8 @604 sin/

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

sw model using - protein search, OM protein September 5, 2004, 09:26:47; Search time 36.5 Seconds (without alignments) 92.892 Million cell updates/sec Run on:

US-09-730-174A-4 61 Title: Perfect score: Sequence:

1 SVSEIQFMHNLG 12

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

368311 Total number of hits satisfying chosen parameters:

1586107 segs, 282547505

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 12

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A\_Geneseq\_29Jan04:\*
1: geneseq11980s:\*
2: geneseq12000s:\*
4: geneseq22001s:\*
5: geneseq22001s:\*
6: geneseq22001s:\*
7: geneseq22003bs:\*
8: geneseq22003bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| SUMMAKIES | pt i (            |      | 608 P | 8969 | AAR91644 Human par | Aay68767 Amino | Aab86219 | Abr44166 Human | 25 Aab86225 Human |      | Aay96981 Parath | Aab86220 | Aay50600 Resin | Aab01862 P |      | 1863 P |      | 1 Aab96931 R | 15 Para | AAB84770 Aab84770 Parathyro | AAB96914 Parathyro | E 69 | 9      | Aar91646 | Antige | 1110 |
|-----------|-------------------|------|-------|------|--------------------|----------------|----------|----------------|-------------------|------|-----------------|----------|----------------|------------|------|--------|------|--------------|---------|-----------------------------|--------------------|------|--------|----------|--------|------|
|           | Length DB         | 11 6 | ā     | 11 3 | 0                  | 0              | 0        | 0              |                   |      |                 | 9        |                |            |      |        | 0    |              | 11 4    |                             |                    |      | m<br>o |          |        |      |
| % (       | Query<br>Match Le | 8    |       | S    | •                  | 73.8           | 73.8     | 73.8           | 67.2              | 63.9 | 63.9            | 63.9     | 63.1           | 59.0       | 59.0 | 54.1   | 54.1 | 54.1         | 54.1    | 54.1                        | 4.                 | 4    | ά.     |          | 。      |      |
|           | Score             |      |       | 46   |                    |                | 45       |                | 41                |      |                 |          |                |            |      |        | 33   |              |         |                             |                    |      |        |          |        |      |
|           | Result<br>No.     |      | 7     | m    | 4                  | 2              | 9        | 7              | 80                | Q    | 10              | 11       | 12             | 13         | 14   | 15     | 16   | 17           | 18      | 19                          | 20                 | 21   | 22     | 23       | 24     |      |

| Abp71484 Parathyro Abp71485 Parathyro Abd71485 Parathyro Abd71482 Parathyro Abd71482 Parathyro Abd71482 Parathyro Abd71482 Parathyro Aab91864 (Asnio, T Aab96892 Rat parat Abd6918 Rat parat Abd6918 Rat parat Abd6918 Rat parat Abd6918 Human DNA Aar91649 Human DNA Aar91649 Human par Abr4168 Human par Abr4168 Human par Abr4168 Human par Aab900068 N-termina | 1864 PTH(1-<br>7062 PTH-rP |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------|
| 6 ABP71484<br>6 ABP71485<br>6 ABP71485<br>6 ABP71482<br>6 ABP71482<br>1 AAB05547<br>1 AAB05547<br>4 AAB05691<br>5 AAB05091<br>6 AAB05091<br>6 AAB05091<br>7 AAB05091<br>7 AAB05091<br>6 AAB05091<br>7 AAB05091<br>7 AAB05091<br>8 AAB05091<br>9 AAB05091<br>9 AAB05091<br>9 AAB05091<br>9 AAB05091<br>9 AAB05091                                                   | 3 AAB0186<br>3 AAY9706     |
| 0.000004444444444444444444444444444444                                                                                                                                                                                                                                                                                                                             | 42.6                       |
| 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0                                                                                                                                                                                                                                                                                                                              | 4.7                        |

#### ALIGNMENTS

ABG72607 standard; peptide; 11 AA. RESULT 1 ABG72607

ABG72607;

(first entry) 11-FEB-2003

Parathyroid hormone antigenic peptide 2-12.

Human, parathyroid hormone, antigen, hypercalcaemia, osteoporosis, primary hyperparathyroidism, mouse, rat, bovine, porcine, canine. THE STATE OF THE S

Homo sapiens.
Mus sp.
Rattus sp.
Bos taurus.
Sus scrofa.
Canis familiaris.

Location/Qualifiers Key Misc-difference 6 /label= Leu, Phe

US2002110871-A1

15-AUG-2002.

05-DEC-2000; 2000US-00730174.

05-DEC-2000; 2000US-00730174.

(ZAHR/) ZAHRADNIK R J. (LAVI/) LAVIGNE J R.

Zahradnik RJ, Lavigne JR;

WPI; 2003-066685/06.

New parathyroid hormone (PTH) antigenic peptide inducing the formation and isolation of antibodies having an affinity to it, useful for determining bioactive PTH levels in serum, plasma and/or cell culture media.

Claim 1; Page 5; llpp; English.

The invention relates to a new antigenic peptide for inducing the formation and isolation of antibodies having an affinity to it, being

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g
formed from the N-terminus of parathyroid hormone (PTH). Also included are; (1) a method for producing antibodies useful in the determination of PTH levels in a biological sample comprising: (a) providing at least one first peptide antigen comprising a peptide fragment of PTH; (b) administering the first peptide antigen to a host animal to induce antister production; (c) monitoring the antibody produced; (d) isolating antisera produced in the host animal; and (e) selecting antisera produced in the host annimal; and (e) selecting antisera from the isolated antisera produced in the host that is capable of the method; and (3) test kits and analytical procedures used for the determination of bloactive intact PTH utilising (ab). The methods and compositions of the present invention are useful for determining bloactive intact PTH levels in serum, plasma and/or cell culture media. The antigens, antibodies and methods of the present invention, as compared to prior art, have the particular advantages of possessing greater affanity for PTH, and in particular, are designed to have a non-molecular forms of PTH. PTH levels are an important parameter in patients suffering from hypercalcaemia, osteoporosis and primary chapter representing amino acids 2-12 of human, mouse, rat, porcine, canning and bovine PTH
 ö
 0; Gaps
 Human, parathyroid hormone, antigen, hypercalcaemia, osteoporosis, primary hyperparathyroidism, mouse, rat, bovine, porcine, canine.
 82.0%; Score 50; DB 6; Length 11; 90.9%; Pred. No. 0.01;
 1; Indels
 Parathyroid hormone antigenic peptide 1-12.
 0; Mismatches
 Location/Qualifiers
 ABG72608 standard; peptide; 12 AA.
 /label= Ser, Ala
 05-DEC-2000; 2000US-00730174
 /label= Leu,
 05-DEC-2000; 2000US-00730174
 Zahradnik RJ, Lavigne JR;
 (first entry)
 Query Match
Best Local Similarity 90.5
Matches 10; Conservative
 VSEIQFMHNLG 12
 1 VSEIOXMHNLG 11
 (ZAHR/) ZAHRADNIK R J.
(LAVI/) LAVIGNE J R.
 Mus sp.
Rattus sp.
Bos taurus.
Sus scrofa.
Canis familiaris.
 Misc-difference 7
 Misc-difference
 US2002110871-A1
 Sequence 11 AA;
 Homo sapiens.
 11-FEB-2003
 15-AUG-2002.
 ~
 ABG72608;
 RESULT 2
ABG72608
 8
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The invention relates to a new antigenic peptide for inducing the formation and isolation of antibodies having an affinity to it, being formed from the N-erminus of parathyroid hormone (PTH). Also included are; (1) a method for producing antibodies useful in the determination of PTH levels in a biological sample comprising: (a) providing at least one first peptide antigen comprising a peptide fragment of PTH; (b) administering the first peptide antigen to a host animal to induce antibody production; (c) monitoring the antibody titre produced; (d) isolating antisera produced in the host animal to induce antibody production; (c) monitoring the antibody titre produced; (d) isolating antisera produced in the host animal to induce the method; and (3) test kits and analytical procedures used for the determination of bioactive intact PTH ullising (ab). The methods and compositions of the present invention are useful for determining bioactive intact PTH levels in serum, plasma and/or cell culture media. The antigens, antibodies and methods of the present invention, as compared to prior art, have the particular advantages of possessing creagation for mainto acid residues extending beyond the first N-terminal creamining and further have negligible cross-reactivity with the large non-molecular forms of PTH. PTH levels are an important parameter in patients suffering from hypercal acemia, osteoporosis and primary chepting are an important parameter in patient and bovine PTH antigemence represents a PTH antigemic compared to prior after the present sequence represents and primary porcine, canine and bovine PTH
 ·
0
 formation
New parathyroid hormone (PTH) antigenic peptide inducing the formatior and isolation of antibodies having an affinity to it, useful for determining bioactive PTH levels in serum, plasma and/or cell culture
 Gaps
 PTH; parathyroid hormone; N-terminal; signaling domain; bone mass; bone reformation; resorption; remodeling; tetherl; osteoporosis.
 Parathyroid hormone N-terminal signaling domain (residues 1-11).
 ..
 Score 50; DB 6; Length 12; Pred. No. 0.011;
 1; Indels
 0; Mismatches
 AAY96968 standard; peptide; 11 AA.
 Claim 2; Page 5; 11pp; English.
 99WO-US031108.
 98US-0114577P.
 82.0%;
 (first entry)
 82.0
Best Local Similarity 90.9
Matches 10; Conservative
 2 VSEIQXMHNLG 12
 2 VSEIQFMHNLG 12
 (GARD/) GARDELLA T J.
(KRON/) KRONENBERG H M.
(POTT/) POTTS J T.
 40200039278-A2.
 Sequence 12 AA;
 31-DEC-1998;
 30-DEC-1999;
 Homo sapiens
 31-OCT-2000
 06-JUL-2000.
```

```
WO200004047-A1
 Unidentified
 07-JUL-1999;
 17-JUL-1998;
 05-MAY-2000
 27-JAN-2000
 Lintner K;
 Query Match
Best Local S
Matches 9
 AAY68767;
 Н
 AAY68767
 RESULT 5
 AAY68767
 g
 88666666
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 à
 염
 Compounds of the structure or formula S-(L) n-B, R.1-S-(L) n-R or S-(L) n-R are new. S is an amino terminal signaling functional domain of parathyroid hormone (PTH), L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R i is the PTH-I receptor signal sequence; and R is (a portion of) PTH-1 receptor sequence. The new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone reformation, bone resorption and/or bone remodeling, treating diseases and disorders associated with decreased tetherl activity, increasing cAMP in a mammalian cell having PTH-1 receptors, or screening for a peptide or inhalation unlike the large native PTH or PTH-PTH administered by regular injections to treat osteoporosis
 ö
 human parathyroid hormone - and antibodies distinguish between active and inactive
 New compound comprising an amino terminal signaling functional domain
linked to a carboxy-terminal binding portion of parathyroid hormone for
treating mammalian conditions characterized by decreases in bone mass.
 Gaps
 hormone; hPTH; antigen; alpha-helix; immunogen;
 .
0
 DB 3; Length 11;
0.059;
 1; Indels
 Human parathyroid hormone antigenic peptide hPTH 1-10.
 Jueppner H;
 Maegerlein M;
 1; Mismatches
 Score 46;
Pred. No. (
 Potts JT,
 ů,
 AAR91644 standard; peptide; 10 AA.
 Claim 4; Page 92; 119pp; English
 Hock
 (s) from able to
 Gardella TJ, Kronenberg HM,
 94DE-04434551
 94DE-04434551
 German
 75.4%;
 Human parathyroid hormone; I diagnosis; active hPTH 1-37
 3
 (first entry)
 New antigenic peptide(s) generated using them, abl forms of the hormone.
 9; Conservative
 1 AVSEIQLMHNL 11
 1 SVSEIQFMHNL 11
 Forssmann
 Claim 2; Page 4; 5pp;
 (FORS/) FORSSMANN W.
 WPI; 1996-180391/19.
 WPI; 2000-452384/39
JUEPPNER H.
 Query Match
Best Local Similarity
Matches 9; Conserv
 Sequence 11 'AA;
 DE4434551-A1.
 28-SEP-1994;
 28-SEP-1994;
 06-NOV-1996
 Adermann K,
 04-APR-1996
 AAR91644;
(JUEP/)
 RESULT 4
AAR91644
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O
The present sequence is a specific example of claimed immunogenic peptides having a sequence from hPTH(1-37) which includes the N- or C-terminal alpha-helical region and/or the non-structured region of the hormone. Antibodies and their binding fragments generated by injecting an animal with the peptides are useful as diagnostic reagents for determination of biologically active hPTH(1-37)
 The present sequence represents a parathyroid hormone (pTH) fragment, comprising amino acids 1-10. Parathyroid hormone fragments of the invention have lipolysis stimulating activity (especially when topically administered). The lipolytic activity of the peptides is enhanced when they are chemically modified to increase their lipophilicity. The peptides are used in cosmetic or dermatological compositions for skin care. They are especially used for slimming treatment of excessive weight in the thighs and hips, in the treatment of cellulite and for skin
 used as lipolysis stimulants for slimming treatment of
 Gaps
 Gaps
 Parathyroid hormone, lipolysis, cosmetic, dermatological, skin care, slimming treatment, cellulite, skin firming.
 ·.
 .
0
 Length 10;
 Length 10
 1; Indels
 Amino acids 1-10 of a parathyroid hormone (pTH)
 Score 45; DB 3;
Pred. No. 0.082;
); Mismatches
 Score 45; DB 2;
Pred. No. 0.082;
0; Mismatches
 New parathyroid hormone fragment peptides, in topically applied cosmetic compositions excessive weight in hips and thighs.
 Ą.
 .
 10
 Claim 1; Page 8; 18pp; French
 99WO-FR001687.
 73.8%;
90.0%;
 98FR-00009193.
 73.8%;
90.0%;
 standard; peptide;
 (first entry)
 Query Match
Best Local Similarity 90.0
Local Similarity 90.0
 Similarity 90.0
 1 SVSEIQFMHN 10
 SVSEIQLMHN 10
 SVSEIQFMHN 10
 SVSEIOLMHN 10
 WPI; 2000-171243/15.
 (SEDE-) SEDERMA
 Sequence 10 AA;
 Sequence 10 AA;
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AAB86219;

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Novel fusion peptide comprising self cell-penetrating Tat peptide bound to human parathyroid hormone-derived peptide, useful as component of skin slimming cosmetic composition.
 The invention relates to a fusion peptide (Tat-hPTHDP), where self cellpenetrating Tat peptide is bound to human parathyroid hormone-darived peptide (hPTHDP). The fusion peptide is useful as a component of skin slimming cosmetic composition. The fusion peptide does not cause irritation, easily and safely penetrates into integument and endothelium, does not cause skin disease and has superior lipolysis effects, and is durable. The present sequence represents a human parathyroid hormone (hPTH) fragment that can be used to construct the fusion peptide
 Fusion peptide, tat, hPTHDP; parathyroid hormone; skin, cosmetic, lipolysis; human; hPTH.
 Parathyroid hormone; hPTH; immunogenic peptide; human; epitope; diagnosis; calcium-metabolism disorder; osteopathy; antagonist; hypo-parathyroidism; hyper-parathyroidism.
 Human parathyroid hormone (hPTH) fragment (residues 1-10).
 73.8%; Score 45; DB 6; Length 10; 90.0%; Pred. No. 0.082;
 Human parathyroid hormone immunogenic peptide SEQ ID 7.
 Kang S,
 Mismatches
 (GLDS) LG HOUSEHOLD & HEALTH CARE LTD.
 Cho W,
 AAB86225 standard, peptide, 9 AA.
 Claim 5; Page 6; 32pp; English
 27-SEP-2001; 2001KR-00060245.
15-MAR-2002; 2002KR-00014062.
 06-MAY-2002; 2002WO-KR000835
(first entry)
 (first entry)
 Kang N, Park S,
 Conservative
 1 SVSEIQFMHN 10
 WPI; 2003-468288/44.
 SVSEIQLMHN
 Local Similarity
 WO2003035697-A1.
 Sequence 10 AA;
 DE19961350-A1
 Homo sapiens
04-AUG-2003
 03-SEP-2001
 01-MAY-2003
 .
.
 AAB86225;
 Query Match
 Chang M;
 Song Y,
 Best Loc
Matches
 AAB86225
 RESULT
8
 characteristics a liver interior to the transfer of active parathyzoid hormone (A) by treating a sample with (i) antibody (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A). The including the N-terminal residue and (ii) antibody (Ab2) that recognizes an epitope within the receptor-binding site of (A). The number of molecules that react with both antibodies is determined and used to calculate the content of physiologically active (A). The method is used for diagnosis of calcium-method (unlike known assays) recognizes that (i) some fragments of (A) shorter than the complete (B4 aa) peptide are (i) some fragments of (A) shorter than the complete (B4 aa) peptide are cartagonistic (these have the receptor-binding site but lack the N-terminus). It thus provides a true measure of the content of physiologically active (A); contrast methods that measure intact peptide and its 1-37 fragment which may produce falsely high values. This sequence represents a peptide fragment used to illustrate the method of
 ô
 Determining the content of physiologically active parathyroid hormone, useful in diagnosis of calcium-metabolism disorders, using two antibodies reactive with different epitopes.
 This invention describes a novel method for determining (MI) the content
 Gaps
 Parathyroid hormone, hPTH, immunogenic peptide, human, epitope, diagnosis, calcium-metabolism disorder, osteopathy, antagonist, hypo-parathyroidism, hyper-parathyroidism.
 ö
 Score 45; DB 4; Length 10;
Pred. No. 0.082;
0; Mismatches 1; Indels
 Human parathyroid hormone immunogenic peptide SEQ ID 1.
 ABR44166 standard; peptide; 10 AA.
 AAB86219 standard; peptide; 10 AA.
 Disclosure; Page 3; 10pp; German.
 99DE-01061350
 99DE-01061350
 73.8%;
90.0%;
 (IMMU-) IMMUNDIAGNOSTIK AG.
 (first entry)
 Query Match
Best Local Similarity 90.0
Matches 9; Conservative
 9
 1 SVSEIQFMHN 10
 WPI; 2001-376318/40.
 SVSEIQLMHN
 Sequence 10 AA;
 DE19961350-A1
 17-DEC-1999;
 17-DEC-1999;
 03-SEP-2001
 21-JUN-2001
```

AAB86219
AAB

.; 0

Gaps

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1; Indels

99DE-01061350,

17-DEC-1999;

ABR44166;

ABR44166
ID ABR4
XX
AC ABR4

RESULT 7

à

Min H;

Lim J,

Lee Y,

antibodies

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(GARD/)
 (JUEP/)
 (KRON/)
 RESULT 10
 AAY96981
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 a
 This invention describes a novel method for determining (MI) the content of active parathyroid hormone (A) by treating a sample with (I) antibody (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A), and including the N-terminal residue and (II) antibody (Ab2) that recognizes an epitope within the receptor-binding site of (A). The number of molecules that react with both antibodies is determined and used to calculate the content of physiologically active (A). The method is used for diagnosis of calcium-metabolism disorders, osteopathy, or hypo- or hyper-parathyroidism. The method (unlike known assays) recognizes that (I) some fragments of (A) shorter than the complete (84 aa) peptide are active and (ii) that apparently intact peptide may be biologically are antagonistic (these have the receptor-binding site but lack the N-terminus). It thus provides a true measure of the content of the content of physiologically active (A); contrast methods that measure intact peptide and its 1-37 fragment which may produce falsely high values. This sequence represents a peptide fragment used to illustrate the method of
 ö
 Determining the content of physiologically active parathyroid hormone, useful in diagnosis of calcium-metabolism disorders, using two antibodies reactive with different epitopes.
 Gaps
 hormone; hPTH; antigen; alpha-helix; immunogen;
 .;
0
 Score 41; DB 4; Length 9; Pred. No. 1.4e+06; 0; Mismatches 1; Indels
 Human parathyroid hormone antigenic peptide hPTH 1-9.
 Maegerlein M;
 à
 AAR91645 standard; peptide; 9 AA.
 Disclosure, Page 3; 10pp; German
 Hock
 ;
0
 67.2%;
88.9%;
 94DE-04434551,
 94DE-04434551,
 diagnosis; active hPTH 1-37.
 (IMMU-) IMMUNDIAGNOSTIK AG
 Forssmann W,
 (first entry)
 8; Conservative
 2 VSEIQFMHN 10
 ഗ
 WPI; 2001-376318/40.
 (FORS/) FORSSMANN W.
 WPI; 1996-180391/19
 VSEIOLMHN
 Best Local Similarity
Matches 8; Conser
 Human parathyroid
 Sequence 9 AA;
 Armbruster FP
 the invention
 17-DEC-1999;
 DE4434551-A1
 28-SEP-1994;
 28-SEP-1994;
 06-NOV-1996
 04-APR-1996
 Adermann K,
 Synthetic.
 AAR91645;
 Query Match
 RESULT 9
셤
 ò
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ô
 The present sequence is a specific example of claimed immunogenic peptides having a sequence from hPTH(1-37) which includes the N- or C-terminal alpha-helical region and/or the non-structured region of the hormone. Antibodies and their binding fragments generated by injecting an animal with the peptides are useful as diagnostic reagents for determination of biologically active hPTH(1-37)
 Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or S-(L)_n-R, are new. S is an amino terminal signaling functional domain of parathyroid hormone (PTH); L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R 1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor sequence. The new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone reformation, bone resopption and/or bone remodeling tracts of bone and disorders associated with decreased tetherl activity, increasing cAMP in a mammalian cell having PTH-1 receptors, or screening for a peptide or
 New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyzoid hormone for treating mammalian conditions characterized by decreases in bone mass.
New antigenic peptide(s) from human parathyroid hormone - and antibod.
generated using them, able to distinguish between active and inactive
 Gaps
 PTH; parathyroid hormone; N-terminal; signaling domain; bone mass; bone reformation; resorption; remodeling; tether1; osteoporosis.
 0
 Score 39; DB 2; Length 9;
Pred. No. 1.4e+06;
0; Mismatches 1; Indels
 Jueppner H;
 Parathyroid hormone N-terminal signaling domain.
 Potts JT,
 Claim 11; Page 93; 119pp; English.
 AAY96981 standard; peptide; 9 AA.
 Page 4; Spp; German.
 99WO-US031108.
 Gardella TJ, Kronenberg HM,
 98US-0114577P
 63.9%;
 (first entry)
 Query Match
Best Local Similarity 88.2
Local 8; Conservative
 generated using them, forms of the hormone.
 GARDELLA T J.
KRONENBERG H
 σ
 WPI; 2000-452384/39.
 JUEPPNER H.
 SVSEIQFMH
 SVSEIOLMH
 WO200039278-A2
 Sequence 9 AA;
 Homo sapiens
 30-DEC-1999;
 31-DEC-1998;
 31-OCT-2000
 06-JUL-2000
 Claim 2;
 Н
 AAY96981;
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. 0

Gaps

.,

Indels

Pred. No. 1.4e+06; 0; Mismatches 1;

88.98;

Similarity 88,9 8; Conservative

Best Local Matches

σ

1 SVSEIOFMH 1 SVSEIQLMH

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AAY50600 standard; peptide; 11 AA.

RESULT 12 AAY50600

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Resin bound cyclic peptide 33.

(first entry)

09-FEB-2000

AAY50600;

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This invention describes a novel method for determining (MI) the content of active parathyzoid hormone (A) by treating a sample with (i) antibody (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A), and including the N-terminal residue and (ii) antibody (Ab2) that recognizes an epitope within the receptor-binding site of (A). The number of molecules that react with both antibodies is determined and used to calculate the content of physiologically active (A). The method is used for diagnosis of calcium-metabolism disorders, ostoopathy, or hypo- or hyper-parathyroidism. The method (unlike known assays) recognizes that (i) some fragments of (A) shorter than the complete (B4 aa) peptide are active and (ii) that apparently intact peptide may be biologically are antagonistic (these have the receptor-binding site but lack the N-terminus). It thus provides a true measure of the content of the con
non-peptide PTH (claimed). The new compound can be administered by inhalation unlike the large native PTH or PTHrP which avoids the need for regular injections to treat osteoporosis
 Determining the content of physiologically active parathyroid hormone, useful in diagnosis of calcium-metabolism disorders, using two antibodies
 Gaps
 Parathyroid hormone; hPTH; immunogenic peptide; human; epitope; diagnosis; calcium-metabolism disorder; osteopathy; antagonist; hypo-parathyroidism; hyper-parathyroidism.
 ö
 Score 39; DB 3; Length 9;
Pred. No. 1.4e+06;
0; Mismatches 1; Indels
 Human parathyroid hormone immunogenic peptide SEQ ID 2.
 AAB86220 standard; peptide; 9 AA.
 reactive with different epitopes.
 Disclosure; Page 3; 10pp; German
 63.98;
88.98;
 99DE-01061350.
 99DE-01061350
 (IMMU-) IMMUNDIAGNOSTIK AG.
 03-SEP-2001 · (first entry)
 Conservative
 σ
 σ
 WPI; 2001-376318/40.
 Best Local Similarity
Matches 8; Conserv
 1 SVSEIQFMH
 SVSEIQLMH
 Armbruster FP;
 Sequence 9 AA;
 DE19961350-A1
 Homo sapiens
 17-DEC-1999;
 17-DEC-1999;
 21-JUN-2001.
 AAB86220;
 Query Match
 AAB86220

XX

AAB8

XX

XX

XX

XX

AAB8

XX

XX

ABB

XX

XX

ABB

XX

ABB

 RESULT 11
 82838
 g
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This invention describes a novel method for the preparation of peptides (II) that contain both cyclic and linear peptide fragments comprises sequential reaction of a resin-bound linear fragment with the cyclic fragment in N-protected form and optionally other linear fragments. The products of the invention have osteopathic and hypotensive activity. (II) bind to hPPH receptors and act as agonists or antagonists of hPPH. The parathyroid hormone (PTH) or PTH-related peptide analogs of parathyroid hormone (PTH) or PTH-related peptides which are useful for treating diseases that respond to treatment with agents that bind to PTH receptors (with or without activation of adenyly) cyclase activity), e.g. byper- or hypo-calcemia, osteoporosis, osteopenia, hyper- or hypo-calcemia, osteoporosis, osteopenia, hyper- or hypo-calcemia, osteoporosis, osteopenia, hyper- or hypo-calcemia, cushing's syndrome, renal failure and hypertension, also for promoting repair of bone fractures. Separate synthesis of the cyclic fragment allows convergent synthesis of resin-bound (II), with better yields and higher throughput. The difficulties associated with preparation of the bridged fragment are confined to a small peptide which
 Cyclic peptide; resin bound; parathyroid hormone; osteopathic; disease hypotensive; PTH receptor; treatment; hypotraclicemia; hypotroalis; osteopenia; hypotraparathyroidism; hypotroathyroidism; custooporosis; osteopenia; hypotraparathyroidism; hypotraparathyroidism; cushing's syndrome; renal failure; hypertension; bone fracture repair.
 Convergent synthesis of peptides for treating e.g. bone disorders
 RHON) RHONE-POULENC RORER PHARM INC.
 Location/Qualifiers
 Disclosure; Page 75; 85pp; English.
 "Ser(OtBu)"
 /note= "FMOC-Ala"
 "His(Trt)"
 "Asn (Trt) "
 99WO-US008435
 98US-0081897P.
 Mencel JJ;
 'note=
 'note=
 'note=
 /note=
 'note=
 WPI; 1999-633822/54.
 Misc-difference 10
 Misc-difference
 Misc-difference
 Misc-difference
 Misc-difference
 Misc-difference
 Sledeski AW,
 15-APR-1999;
 15-APR-1998;
 W09952933-A1
 21-OCT-1999
 Synthetic
```

63.9%; Score 39; DB 4; Length 9;

Query Match

the invention

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The invention relates to a novel parathyroid hormone (PTH) peptide

(AAB01859) and parathyroid hormone-related peptide (PTHTP, AAB01860), and
blologically active derivatives thereof (AAB01857-B01858, AAB01861).

(Boll869). The peptides of the invention are at least 85% identical to the
generic peptide of the formula: XI val-Ser-Glu-X2-Gln-Leu-X3-His-X4-X5-
CG Gly-Lys-X6 (AAB01857) where: XI is Ser or Ala; X2 is Ile or Lys; X3 is
Met, Leu or Nle; X4 is Asn or Asp; X5 is Leu or Lys; X6 is His or Ser;
provided that the peptide is not PTHFF(1-14). The peptides of the
invention also encompass fragments of peptides of the invention
consisting of maino acids 1-9, 1-10, 1-11, 1-12 and 1-13, and N- and C-
cerminal derivatives. PTH is a major regulator of calcium homeostasis,
and is necessary for the normal function of the gastrointestinal,
consisting to both PTH-1 receptors on osteoblasts and renal tubular cells,
and to the recently identified PTH-2 receptor. PTH has a potent anabolic
ceffect on the skeleton, and mediates calcium reabsorption, enhances
consisting of protein hormones, the PTH-related proteins (PTHFP) mimic some of
the renal and skeletal actions of PTH, and also bind to the PTH-1
 ;
;
can be purified before reaction with the resin-bound component. AAY50568-Y50614 represent the peptide fragments described in the method of the invention
 Parathyroid hormone (FTH) peptides, FTH related peptides and the nucleic acids that encode them, useful for treating osteoporosis.
 Gaps
 Parathyroid hormone peptide, PTH, PTH-related peptide, PTHrP, calcium homeostasis, PTH-1 receptor; PTH-2; vitamin D synthesis, bone synthesis; agonist, osteoporosis; non-parenteral delivery.
 :
 Length 11;
 Indels
 Jueppner H;
 PTH(1-14)/PTHrP(1-14)-derived peptide, SEQ ID NO:6.
 Score 38.5; DB 2;
Pred. No. 1.5;
2; Mismatches 0;
 Potts JT,
 Disclosure; Page 26; 73pp; English.
 AAB01862 standard; peptide; 9 AA.
 Gardella TJ, Kronenberg HM,
 63.1%;
 99WO-US024481.
 98US-0105530P
 Query Match
Best Local Similarity 75.00,
Best Local 9, Conservative
 11-SEP-2000 (first entry)
 1 SVSEIQFMHNLG 12
 1 AVSEIQ-LHNLG 11
 (GARD/) GARDELLA T J.
(KRON/) KRONENBERG H M.
(POTT/) POTTS J T.
 WPI; 2000-339693/29.
 (JUEP/) JUEPPNER H.
 Sequence 11 AA;
 WO200023594-A1.
 sapiens.
 20-OCT-1999;
 22-OCT-1998;
 27-APR-2000.
 Synthetic
 AAB01862;
 RESULT 13
AAB01862
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 Compounds of the structure or formula S-(L) n-B, R l-S-(L) n-R or S-(L) n-R, are new. S is an amino terminal signaling functional domain of parathyroid hormone (PTH); L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R l is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor sequence. The new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone reformation, bone resorption and/or bone remodeling, treating diseases
 invention are either agonists of PTH-1 and PTH-2 receptors (AAB01885), AAB01861-B01865) or are PTH-1/PTH-2 receptor antagonists (AAB01867-B01869). PTH-1/PTH-2 receptor antagonists are useful for the treatment of conditions characterised by a decrease in bone mass, such as casteoporosis. PTH-1/PTH-2 receptor antagonists are useful for treating medical disorders that arise from excessive or altered action of the PTH-1/PTH-2 receptor. Detectably labelled peptides of the invention are also useful in the determination of rates of bone formation, bone resorption and/or bone remodelling in a patient. The peptides of the invention are "minimised" versions of PTH or PTH-P which are inexpensive to prepare by conventional synthetic chemistry, and can be delivered to a patient via non-parenteral routes. Sequences AAB01858 and AAB01861-B01866 represent
 New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass.
 Gaps
 parathyroid hormone, N-terminal; signaling domain; bone mass; reformation; resorption; remodeling; tether1; osteoporosis.
 Parathyroid hormone N-terminal signaling domain (residues 1-9).
 .
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 Score 36; DB 3; Length y;
Pred. No. 1.4e+06;
 Potts JT, Jueppner H;
receptor. They do not bind to the PTH-2 receptor.
 Claim 4; Page 92; 119pp; English.
 AAY96966 standard; peptide; 9 AA.
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 59.0%;
77.8%;
 Sardella TJ, Kronenberg HM,
 99WO-US031108
 98US-0114577P
 31-OCT-2000 (first entry)
 Conservative
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 GARDELLA T J. KRONENBERG H
 Query Match
Best Local Similarity
7; Conserve
 WPI; 2000-452384/39.
 JUEPPNER H.
 1 SVSEIQFMH
 1 AVSEIQLMH
 WO200039278-A2
 Sequence 9 AA;
 31-DEC-1998;
 30-DEC-1999;
 Homo sapiens
 06-JUL-2000.
 AAY96966;
 (KRON/)
(POTT/)
 (GARD/)
 (JUEP/)
 PTH;
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The invention relates to a novel parathyroid hormone (PTH) peptide

(AAB01859) and parathyroid hormone-related peptide (PTHPP; AAB01860), and
biologically active derivatives thereof (AAB01856, AAB01861)

(Biologically active derivatives thereof (AAB01856, AAB01861)

(Biologically active derivatives thereof (AAB01856, AAB01861)

(Gly-Lys-X6 (AAB01857) where X1 is Ser or Ala; X2 is Ile or Lys: X4-X5-

(Gly-Lys-X6 (AAB01857) where X1 is Ser or Ala; X2 is Ile or Lys: X3 is

Met, Leu or NIe; X4 is Asn or A89; X5 is Leu or Lys; X6 is His or Ser;

provided that the peptide is not PTHPP(1.14). The peptides of the
invention also encompass fragments of peptides of the invention

consisting of amino acids 1-9, 1-10, 1-11, 1-12 and 1-13, and N- and C-

terminal derivatives. PTH is a major regulator of calcium homeostasis,

and is necessary for the normal function of the gastrointestinal,

skeletal, neurological system, neuromiscular and cardiovascular systems.

It binds to both PTH-1 receptors on osteoblasts and renal tubular cells,

and the skeleton, and mediates calcium reabsorption, enhances

phosphate clearance and vitamin D synthesis in the kidney. A homologous
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and disorders associated with decreased tetherl activity, increasing CAMP in a mammalian cell having PTH-1 receptors, or screening for a peptide or non-peptide PTH (claimed). The new compound can be administered by inhalation unlike the large native PTH or PTHrP which avoids the need for regular injections to treat osteoporosis
 Parathyroid hormone (PTH) peptides, PTH related peptides and the nucleic acids that encode them, useful for treating osteoporosis.
 Gaps
 Parathyroid hormone peptide, PTH, PTH-related peptide, PTHrP; calcium homeostasis, PTH-1 receptor; PTH-2; vitamin D synthesis; bone synthesis; agonist; osteoporosis; non-parenteral delivery.
 .
 Score 36; DB 3; Length 9;
Pred. No. 1.4e+06;
1; Mismatches 1; Indels
 Jueppner H;
 PTH(1-14)/PTHrP(1-14)-derived peptide, SEQ ID NO:7.
 Potts JT,
 Disclosure; Page 26; 73pp; English.
 AAB01863 standard; peptide; 9 AA
 Kronenberg HM,
 59.0%;
 99WO-US024481.
 98US-0105530P
 11-SEP-2000 (first entry)
 Conservative
 GARDELLA T J.
KRONENBERG H M.
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 1 AVSEIQLMH 9
 Query Match
Best Local Similarity
 POTTS J T.
JUEPPNER H.
 WPI; 2000-339693/29
 SVSEIQFMH
 WO200023594-A1.
 Sequence 9 AA;
 sapiens.
 20-OCT-1999;
 22-OCT-1998;
 Gardella TJ,
 27-APR-2000.
 Synthetic.
 AAB01863;
 (POTT/)
 (GARD/)
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calls of protein hormones, the PTH-related proteins (PTHrP) minic some of the renal and skeletal actions of PTH, and also bind to the PTH-1 creceptor. They do not bind to the PTH-1 receptor. The peptides of the invention are either agonists of PTH-1 and PTH-2 receptors (AAB01856, AAB01861-B01866) or are PTH-1/PTH-2 receptor antagonists (AAB01867-S01869). PTH-1/PTH-2 receptor agonists are useful for the treatment of conditions characterised by a decrease in bone mass, such as osteoporosis. PTH-1/PTH-2 receptor antagonists are useful for treating medical disorders that arises from excessive or altered action of the PTH-1/PTH-2 receptor. Detectably labelled peptides of the invention are also useful in the determination of rates of bone formation, bone resorption and/or bone remodelling in a patient. The peptides of the invention are and/or bone remodelling in a patient. The peptides of the invention are minimised" versions of PTH or PTHFP which are inexpensive to prepare by conventional synthetic chemistry, and can be delivered to a patient via
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 Gaps
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 Mismatches
 5, 2004, 09:34:30
 PTH-1/PTH-2 receptor agonists
 54.1%;
66.7%;
 Local Similarity 66.7
les 6; Conservative
 Search completed: September
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1 AVSEIQLLH
 1 SVSEIQFMH
 Job time : 36.5 secs
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Sequence 4, Appli
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Sequence 7, Appli
Sequence 7, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 61, Appli
 September 5, 2004, 09:37:09; Search time 32.5 Seconds (without alignments) 116.332 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Description
 Published Applications And Comparations of Comparations and Comparations a
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 US-09-730-174A-4
US-09-730-174A-4
US-09-730-174A-2
US-09-730-174A-3
US-09-730-174A-3
US-09-730-174A-1
US-10-168-185-1
US-10-168-185-7
US-10-168-185-7
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 Total number of hits satisfying chosen parameters:
 1298764 seqs, 315065143 residues
 SUMMARIES
 Published Applications AA:*
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
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 1 SVSEIQFMHNLG 12
 US-09-730-174A-4
61
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| US-10-168-185-4<br>US-10-168-185-4<br>US-10-168-185-18<br>US-10-108-185-18<br>US-10-137-867-52<br>US-09-834-765-54<br>US-09-834-765-78<br>US-09-834-765-78<br>US-09-834-765-78<br>US-09-834-765-78<br>US-10-153-187-8<br>US-10-153-187-8<br>US-10-153-187-8<br>US-10-153-187-8<br>US-10-153-187-8<br>US-10-153-187-8<br>US-10-153-187-8<br>US-10-167-147-140-26<br>US-10-024-652-13<br>US-10-024-652-13<br>US-10-024-652-13<br>US-10-024-652-13 | US-10-024-652-105<br>US-10-024-652-138<br>US-10-024-652-146<br>US-10-024-652-205<br>US-00-024-652-205<br>US-09-976-787-4<br>US-09-965-198-4<br>US-09-965-099-12 |
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#### ALIGNMENTS

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Sequence 4, Application US/09730174A

Percent No. US20020100971AI

Sequence 4, Application US/09730174A

Percent No. US20020100971AI

Settle No. US20020100971AI

Settle No. US200201100971AI

TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid H.

FILE REPRENCE: INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid H.

CURRENT APPLICATION UNMER: US/09/730,174A

CURRENT FILING DATE: 2000-12-05

NUMBER OF SEQ ID NOS: 12

TYPE: PAT

ORGANIGN: Artificial Sequence

FRATURE:

ORGANIGN: Artificial Sequence

FRATURE:

ORGANIGN: No. 00.0015;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Best Local Similarity 100.0%; Pred. No. 0.00015;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY I SYSEIOFMANIG 12

Best Local Similarity 100.0%; Pred. No. 0.00015;

Matches 12: Conservative 0; Mismatches 0; Indels 0; Caps 0;

TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid H; FILE REFERENCE: INTUNE-001A
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Sequence 1. Application US/09730174A

Patent No. US20020110871A1

GENERAL INFORMATION:

APPLICANT: Zahradanik, R.J.

ITILE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid HO

FILE REFERENCE: IMUNE-001A

CURRENT APPLICATION NUMBER: US/09/730,174A

UNMBER OF SEQ ID NOS: 12
 APPLICANT: Zahradnik, R.J.
TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid HO FILE REPRENCE: IMUNE-001A CTREENT APPLICATION NUMBER: US/09/730,174A CURRENT APPLICATION NUMBER: 2000-12-05 NUMBER OF SEQ ID NOS: 12 SEQ ID NOS: 12
 , OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies US-09-730-174A-5
 FEATURE:
, OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-1
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 83.6%; Score 51; DB 9; Length 11; 90.9%; Pred. No. 0.0097; tive 0; Mismatches 1; Indels
 Score 52; DB 9; Length 12;
Pred. No. 0.0069;
1; Mismatches 1; Indels
 APPLICANT: Armbruster, Franz Paul
APPLICANT: Missbichler, Albert
APPLICANT: Schmidt-Gayk, Heinrich
APPLICANT: Schmidt-Gayk, Heinrich
APPLICANT: Noth, Heinz-Jurgen
TITLE OF INVENTION: Method for Determining Parathormone
 Sequence 5, Application US/09730174A patent No. US20020110871A1 GENERAL INFORMATION:
 Sequence 1, Application US/10168185; Publication No. US20030175802A1; GENERAL INFORMATION:
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Best Local Similarity 83.3%;
Matches 10; Conservative
 ORGANISM: Artificial Sequence
 Best Local Similarity 90.9
Matches 10; Conservative
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 1 SVSEIOFMHNLG 12
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 2 VSEIQFMHNLG 12
 1 VSEIQLMHNLG 11
 US-09-730-174A-5
 RESULT 6
US-09-730-174A-1
 RESULT 7
US-10-168-185-1
 SEO ID NO 1
 IYPE: PRT
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 Sequence 3, Application US/09730174A

Patent No. US20020110871A1

GENERAL INFORMATION:

APPLICATION: Astroduik, R.J.

TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a

TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Hc

CURRENT APPLICATION NUMBER: US/09/730,174A

CURRENT FILING DATE: 2000-12-05

SEQ ID NOS: 12

SEQ ID NO 3

LENGTH: 12
 Sequence 2, Application US/09730174A
Patent No. US20020110871A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Ho
 ; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies US-09-730-174A-2
 FEATURE:
OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
 , OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies US-09-730-174A-6
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 93.4%; Score 57; DB 9; Length 11;
100.0%; Pred. No. 0.00075;
tive 0; Mismatches 0; Indels
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Pred. No. 0.00054;
1; Mismatches 0; Indels
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CURRENT FILING DATE: 2000-12-05
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CURRENT APPLICATION NUMBER: US/09/730,174A CURRENT FILING DATE: 2000-12-05 NUMBER OF SEQ ID NOS: 12
 95.1%;
91.7%;
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 ORGANISM: Artificial Sequence
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Best Local Similarity 91.7
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 11; Conservative
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 1 VSEIQFMHNLG 11
 2 VSEIQFMHNLG 12
 Query Match
Best Local Similarity
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US-09-730-174A-2
 RESULT 4
US-09-730-174A-3
 US-09-730-174A-3
 LENGTH: 12
 SEQ ID NO 6
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 NESOUL 192-673-6
Sequence 6, Application US/10192673
Sequence 6, Application US/10192673
Sequence 6, Application WO. US20030166838A1
GENERAL INFORMATION:
APPLICANT: Kornemberg, Henry
APPLICANT: Fortes, John T.
APPLICANT: Pottes, John T.
APPLICANT: Pottes, John T.
APPLICANT: Pottes, John T.
APPLICANT: Parald
TITLE OF INVENTION: Bloactive Peptides and Peptide Derivatives of TITLE OF INVENTION: Barathyroid Hormone (PTH) and Parathyroid
TITLE OF INVENTION: Hormone-Related Peptide (PTH) and Parathyroid
TITLE OF INVENTION: HORMONER: US/10/192,673
CURRENT APPLICATION NUMBER: US/10/192,673
PRICR APPLICATION NUMBER: U.S. 09/421,379
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 APPLICANT: Arrowalton:
APPLICANT: Arrower: Franz Paul
APPLICANT: Arrower: Albert
APPLICANT: Schmidt-Gayk, Heinrich
APPLICANT: Schmidt-Gayk, Heinrich
APPLICANT: Schmidt-Gayk, Heinrich
APPLICANT: Roth, Heinz-Jurgen
; TITLE OF INVENTION: Method for Determining Parathormone
; TITLE OF INVENTION: Method for Determining Parathormone
; TITLE OF INVENTION: Activity in a Human Sample
; TITLE REFERENCE: HIZ-04040
; TITLE REFERENCE: HIZ-04040
; TITLE OF TOWNER: US/10/168,185
; CURRENT APPLICATION NUMBER: US/10/12911
; PRIOR FILING DATE: 2000-12-18
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
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 CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: PCT/EP00/12911
PRIOR FILING DATE: 2000-12-18
PRIOR PILING DATE: 1090-12-17
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SSOFTWARE: PastSEQ for Windows Version 4.0
LENGTH: 9
 RESULT 10
US-10-168-185-8
; Sequence 8, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
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US-10-168-185-2
 ; ORGANISM: Homo sapiens
US-10-168-185-8
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 1 SVSEIOLMH 9
 3 SEIOFMHN 10
 SEIOLMHN 8
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0
 Gaps
 ;
0
 RESULT 8

US-10-168-185-7

Sequence 7, Application US/10168185

Publication No. US20030175802A1

Publication No. US20030175802A1

APPLICANT: Armbruster, Franz Paul

APPLICANT: Armbruster, Franz Paul

APPLICANT: Roth, Heinz-Jurgen

ITILE OF INVENTION: Method for Determining Parathormone

ITILE OF INVENTION: MOTHORE: 2002-06-17

PRIOR PLING DATE: 2000-12-18

PRIOR PLING DATE: 2000-12-18

PRIOR PLING DATE: 1999-12-17

NUMBER OF SEQ ID NOS: 11

SEQ ID NOS: 11

LENGTH: 2

LENGTH: 2

LENGTH: 2

LENGTH: 2

LENGTH: 2
 Query Match 73.8%; Score 45; DB 14; Length 10; Best Local Similarity 90.0%; Pred. No. 0.11; Matches 9; Conservative 0; Mismatches 1; Indels
 RESULT 9
US-10-168-185-2
Sequence 2, Application US/10168185
Publication No. US20030175802A1
GENERAL INFORMATION:
APPLICANT: Armbruster, Franz Paul
APPLICANT: Missbichler, Albert
APPLICANT: Roth, Heinz-Jurgen
TITLE OF INVENTION: Method for Determining Parathormone
TITLE OF INVENTION: Activity in a Human Sample
FILE REPERENCE: HLZ-004US
CURRENT APPLICATION NUMBER: US/10/168,185
 67.2%; Score 41; DB 14; Length 9; 88.9%; Pred. No. 1.2e+06; tive 0; Mismatches 1; Indels
TITLE OF INVENTION: Activity in a Human Sample FILE REFERENCE: HLZ-004US CURRENT APPLICATION NUMBER: US/10/168,185 CURRENT FILING DATE: 2002-06-17 PRIOR APPLICATION NUMBER: PCT/BP00/12911 PRIOR APPLICATION NUMBER: DE 19961350 PRIOR FILING DATE: 1999-12-17 NUMBER OF SEQ ID NOS: 11 SOFTWARE: PastSEQ for Windows Version 4.0 LENGTH: 10
 Query Match
Best Local Similarity 88.5
Matches 8; Conservative
 1 SVSEIQFMHN 10
 1 SVSEIQLMHN 10
 ; ORGANISM: Homo sapiens
US-10-168-185-1
 TYPE: PRT
ORGANISM: Homo sapiens
 2 VSEIQFMHN 10
 1 VSEIQLMHN 9
 US-10-168-185-7
 ò
 g
```

. 0

Gaps

```
Sequence 61, Application US/10033741
Publication No. US20030049640A1
GENERAL INFORMATION:
APPLICANT: Herman, et al.
TITLE OF INVENTION: Proteins, Genes and Their Use For Diagnosis and Treatment of Vascritte OF INVENTION: Response
FILE REFERENCE: 9195-079
 APPLICANT: Gardella, Thomas J.
APPLICANT: Gardella, Thomas J.
APPLICANT: Aronenberg, Henry
APPLICANT: Tronenberg, Henry
APPLICANT: Tronenberg, Henry
APPLICANT: Ungpert, John T.
TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of TITLE OF INVENTION: Parachyroid Hormone (FTH) and Parachyroid TITLE OF INVENTION: Parachyroid Hormone (FTH) and Parachyroid FILE REFERENCE: 0609.4570002
CURRENT APPLICATION NUMBER: U.S. 09/421,379
PRIOR FILING DATE: 2002.07-11
PRIOR FILING DATE: 1998-10-20
PRIOR FILING DATE: 1998-10-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
 OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: peptide
 0;
 Length 8;
 Score 29; DB 14; Length 9;
Pred. No. 1.2e+06;
1; Mismatches 2; Indels
 1; Indels
 Score 31; DB 14;
Pred. No. 1.2e+06;
FILE REFERENCE: HLZ-004US
CURRENT APPLICATION NUMBER: US/10/168,185
CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: PCT/EP00/12911
PRIOR FILING DATE: 2000-12-18
PRIOR FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
 Mismatches
 CURRENT APPLICATION NUMBER: US/10/033,741
 Sequence 10, Application US/10192673
Publication No. US20030166838A1
GENERAL INFORMATION:
 47.58;
 Query Match
Best Local Similarity 87.5%;
Matches 7; Conservative (
 TYPE: PRT
ORGANISM: Artificial Seguence
 Query Match
Best Local Similarity 66.7
Matches 6; Conservative
 TYPE: PRT
ORGANISM: Homo sapiens
 1 SVSEIQFMH 9
 1 SVSEHOLLH 9
 1 SVSEIQFM 8
 1 SVSEIOLM 8
 US-10-192-673-10
 US-10-192-673-10
 US-10-033-741-61
 US-10-168-185-3
 δ
 q
 Db
 ..
0
 .
0
 Gaps
 APPLICANT: EXCELLENCY, ALGORD TO APPLICANT: EXCELLENCY APPLICANT: APPLICANT: APPLICANT: Dotts, John T. APPLICANT: Juppner, Henry APPLICANT: Juppner, Detts, John T. APPLICANT: Juppner, Detts, John T. TITLE OF INVENTION: Bratchyroid Hormone (PTH) and Parathyroid TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid TITLE OF INVENTION: HORMONE-Related Peptide (PTHLP); FILE REFERENCE: 0609,4570002 05/10/192,673
CURRENT APPLICATION NUMBER: U.S. 09/421,379
PRIOR FILING DATE: 1999-10-20
PRIOR FILING DATE: 1999-10-20
PRIOR FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
 OTHER INFORMATION: Description of Artificial Sequence: synthetic; OTHER INFORMATION: peptide
US-10-192-673-7
 OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: peptide
 Ö
 ;;
 Score 36; DB 14; Length 9; Pred. No. 1.2e+06; 1; Mismatches 1; Indels
 54.1%; Score 33; DB 14; Length 9; 66.7%; Pred: No. 1.2e+06;
 Sequence 3, Application US/10168185
Publication No. US20030175802A1
GENERAL INFORMATION:
APPLICANT: Armbruster, Franz Paul
APPLICANT: Schmidt-Gayk, Heinrich
APPLICANT: Schmidt-Gayk, Heinrich
APPLICANT: Roth, Heinz-Jurgen
TITLE OF INVENTION: Method for Determining Parathormone; TITLE OF INVENTION: Activity in a Human Sample
 2; Mismatches
 PRIOR FILING DATE: 1999-10-20
PRIOR APPLICATION NUMBER: U.S. 60/105,530
PRIOR FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 9
 Sequence 7, Application US/10192673
Publication No. US20030166838A1
GENERAL INFORMATION:
APPLICANT: Gardella, Thomas J.
 ORGANISM: Artificial Sequence
 Query Match
Best Local Similarity 77.8%;
Matches 7; Conservative
 ORGANISM: Artificial Seguence
 Query Match
Best Local Similarity 66.7
Matches 6; Conservative
 1 SVSEIOFMH 9
 : | | | | | : |
1 AVSEIQLLH 9
 1 SVSEIQFMH 9
 1 AVSEIQLMH 9
 RESULT 13
US-10-168-185-3
 US-10-192-673-6
 TYPE: PRT
 FEATURE:
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· 0

Gaps

us-09-730-174a-4.closed.rapb

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·.
 0; Gaps
 Query Match
44.3%; Score 27; DB 14; Length 10;
Best Local Similarity 55.6%; Pred. No. 2.4e+02;
Matches 5; Conservative 2; Mismatches 2; Indels
 Search completed: September 5, 2004, 09:49:38 Job time: 33.5 secs
CURRENT FILING DATE: 2001-12-27
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn version 3.0
SEQ ID NO 61
LENGTH: 10
TYPE: PT
CRGANISH: Home sapiens
US-10-033-741-61
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13 ; Search time 11 Seconds (without alignments) 56.319 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 389414 seqs, 51625971 residues
 2004, 09:32:03
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 US-09-730-174A-4
61
1 SVSEIQFMHNLG 12
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 September
 Minimum DB seq length: 0 Maximum DB seq length: 12
 Title:
Perfect score:
 Scoring table:
 Database :
 Sequence:
 Searched:
 on:
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|           | ipt            | equence 31, | -<br>-           | ام.    | e 6             | Sequence 7, Appli | e<br>G        | e 10,            | 42           | 54        | nce 5,           | equence 4, | ω<br>ω   | 42,           | 42,   | 56,        | 56,           | 17,      | 16,            | 15,      | equence 64, | 14           | e 64,  | 9 13,             | equence 7, | 26,    | 26, | 2                |
|-----------|----------------|-------------|------------------|--------|-----------------|-------------------|---------------|------------------|--------------|-----------|------------------|------------|----------|---------------|-------|------------|---------------|----------|----------------|----------|-------------|--------------|--------|-------------------|------------|--------|-----|------------------|
| SUMMARIES | ID             | -09-442-    | US-08-817-547A-1 | -817-5 | US-09-421-379-6 | -09-421-          | -08-817-547A- | US-09-421-379-10 | 5-08-140-137 | 5460978-3 | US-08-817-547A-5 | -08-817-   | -09-421- | -08-482-228-4 | -08-4 | -177-109A- | -08-687-706-5 | -08-817- | -08-817-547A-1 | -08-817- | -08-748-    | -08-817-547A | -08-97 | US-08-817-547A-13 | ٩          | -07-82 | 9   | US-08-977-221-26 |
|           | DB             | 4           | m                | m      | 4,              | 4                 | ო             | 4                | 7            | 9         | m                | m          | 4        | 7             | m     | 0          | 7             | m        | m              | m        | (1)         | ო            | m      | ო                 | m          | Н      | 7-1 | m                |
|           | Length         | 12          | 10               | Q      | Q               | σ                 | 00            | σv               |              | 11        | 9                | 7          | Q        | 12            | 12    | D.         | Ŋ             | Ŋ        | 9              | 7        | 80          | ω            | 80     | o                 | 10         | σn     | σ   | σ                |
| æ         | Query<br>Match | 75.4        | 73.8             | ω.     | •               | 54.1              |               | 47.5             |              |           | 42.6             | •          | •        | ä             | ä     | o,         |               | o,       | o,             | 9.       | ď.          | φ.           | ď.     | φ.                | σ,         | ۲.     | ۲.  | ۲.               |
|           | Score          | 46          |                  | 39     |                 |                   |               |                  |              |           |                  |            |          |               |       |            |               |          |                |          |             |              |        |                   |            |        |     |                  |
|           | Result<br>No.  | H           | 2                | m      | 4               | Ŋ                 | 9             | 7                | 00           | σ         | 10               | 11         | 12       | 13            | 14    | 15         | 16            | 17       | 18             | 19       | 20          | 21           | 22     | 23                | 24         | 25     | 26  | 27               |

| 26, App           | 26,               | 6                | 6               | 7                 | 12, App           | 49,              | 12,              | 12,              | 108                | 49,              | 'n              | 61, Appl         | H               | 60,              | 83,              | 2, 4            | 14, App           |  |
|-------------------|-------------------|------------------|-----------------|-------------------|-------------------|------------------|------------------|------------------|--------------------|------------------|-----------------|------------------|-----------------|------------------|------------------|-----------------|-------------------|--|
| Sequence          | Sequence          | Sequence         | Seguence        | Sequence          | Sequence          | Sequence         | Sequence         | Sequence         | Sequence           | Sequence         | Sequence        | Sequence         | Seguence        | Seguence         | Sequence         | Sequence        | Sequence          |  |
| US-09-483-831B-26 | PCT-US95-06613-26 | US-08-116-778E-9 | US-08-438-562-9 | US-08-483-528B-97 | US-08-783-853A-12 | US-08-836-561-49 | US-09-280-028-12 | US-09-344-050-12 | US-09-393-385B-108 | US-09-434-122-49 | US-09-091-071-3 | US-09-556-605-61 | US-09-064-750-1 | US-09-556-605-60 | US-08-615-181-83 | US-08-555-579-2 | US-08-428-257A-14 |  |
| 4,                | S                 | 2                | ~               | ~                 | ო                 | m                | m                | 4                | 4                  | 4                | 4               | 4                | ო               | 4                | Н                | ч               | 0                 |  |
| σ                 | Q                 | 10               | 10              | 10                | 10                | 10               | 10               | 10               | 10                 | 10               | 10              | 11               | 12              | 12               | 10               | 10              | 10                |  |
| 37.7              | 37.7              | 37.7             | 37.7            | 37.7              | 37.7              | 37.7             | 37.7             | 37.7             | 37.7               | 37.7             | 37.7            | 37.7             | 37.7            | 37.7             | 36.1             | 36.1            | 36.1              |  |
| 23                | 23                | 23               | 23              | 23                | 23                | 23               | 23               | 23               | 23                 | 23               | 23              | 23               | 23              | 23               | 22               | 22              | 22                |  |
| 28                | 29                | 30               | 31              | 32                | 33                | 34               | 35               | 36               | 37                 | 38               | 39              | 40               | 41              | 42               | 43               |                 | 45                |  |

#### ALIGNMENTS

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Sequence 31, Application US/09442889
Sequence 31, Application US/09442889
Sequence 31, Application US/09442889
Sequence 31, Application US/09442889
GENERAL INFORMATION:
APPLICANT: Sledeski, Adam W.
APPLICANT: Mencel, James J.
ITILE OF INVENTION: PEPTIDES
FILLE REPERENCE: A31138-US/09/442,989
CURRENT APPLICATION NUMBER: US/09/442,989
CURRENT FILING DATE: 1999-11-18
BARLIER PHILING DATE: 1999-11-18
NUMBER OF SEQ ID NOS: 46
SOTWARE: Patentin Ver. 2.1
IENGTH: 12
 TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: PEPTIDE
COCATION: (1)
OTHER INFORMATION: FMOC-Ala
FEATURE:
NAME/KEY: PEFTIDE
COCATION: (3)
OTHER INFORMATION: Ser (OLBU)
FEATURE:
 NAME/KEY: PEPTIDE
LOCATION: (4)
OTHER INFORMATION: Glu(OcEu)
 Gln (Trt)
 Asn (Trt)
 His (Trt)
 FEATURE:
NAME/KEY: MOD_RES
LOCATION: (8)
CTHER INFORMATION: NIe
US-09-442-989-31
 LOCATION: (9)
OTHER INFORMATION:
 LOCATION: (10)
OTHER INFORMATION:
 OTHER INFORMATION:
 FEATURE:
NAME/KEY: PEPTIDE
 NAME/KEY: PEPTIDE
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```
Sequence 6, Application US/09421379
Sequence 6, Application US/09421379
Patent No. 649562
GENERAL INFORMATION:
APPLICANT: Gardella, Thomas J.
APPLICANT: Potts, Unn T.
APPLICANT: Potts, Unn T.
APPLICANT: Potts, Unn T.
APPLICANT: Potts, Unn T.
TILE OF INVENTION: Bloactive Peptides and Peptide Derivatives of TITLE OF INVENTION: Hormone-Related Peptide (PTH) and Parathyroid TITLE OF INVENTION: Hormone-Related Peptide (PTH) processed in TITLE OF INVENTION: Hormone-Related Peptide (PTH) and Parathyroid TITLE OF INVENTION: Hormone-Related Peptide (PTH)
FILE REFERENCE: 6060, 4570001
CURRENT FILING DATE: 1999-10-20
CURRENT FILING DATE: 1999-10-20
BARLIER FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIN Ver. 2.0
SERVINARE: PatentIN Ver. 2.0
SERVINARE: PatentIN Ver. 2.0
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic; CTHER INFORMATION: peptide US-09-421-379-6
 Score 39; DB 3; Length 9; Pred. No. 3e+05;
 SIRED: LITE COUNTY: USA

COUNTY: USA

ZITY: Georgia

COMPTER READABLE FORM:
MEDLUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: BATENIT NR-lease #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,547A
FILING DATE:
PRIOR APPLICATION NUMBER: PCT/EP95/03757
FILING DATE:
APPLICATION NUMBER: 29 25PT 1994
ATTORNEY/ACENT INFORMATION:
NAME: FROST, ROGER T:
REGISTRATION NUMBER: 07826-0007
TELEPHONE: 404-818-3709
INFORMATION OR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LEMETHOR A A A SILE STICE:
LEMETHOR A A A SILE STICE:
LEMETHOR A A A SILE STICE:
LEMETHOR A
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Onces & Askew, LLP
STREET: 191 Peachtree Street, 37th Floor
 0; Mismatches
 TYPE: PRT
ORGANISM: Artificial Sequence
 Query Match
Best Local Similarity 88.9%;
Matches 8; Conservative
 9 amino acids
 1 SVSEIQFMH 9
 1 SVSEIQLMH 9
 unknown
 amino acid
 TOPOLOCITYPE: Pe
 STRANDEDNESS:
 HYPOTHETICAL:
 US-08-817-547A-2
 RESULT 4
US-09-421-379-6
 FEATURE:
 g
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 ö
 Gaps
 6
 Score 46; DB 4; Length 12;
Pred. No. 0.013;
1; Mismatches 2; Indels
 DB 3; Length 10;
 GENERAL INFORMATION:
APPLICANT: Adermann, Knut
APPLICANT: Adermann, Knut
APPLICANT: Magerlein, Markus
TITLE OF INVENTION: Peptides from the hPTH Sequence
NUMBER OF SEQUENCES: 36
CORRESPONDENCE 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew, LLP
 APPLICANT: Adermann, Knut
APPLICANT: Hock, Dieter
APPLICANT: Magerlein, Markus
TITLE OF INVENTION: Peptides from the hPTH Sequence
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,547A FILING DATE:
 73.8%; Score 45; DB 3; 90.0%; Pred. No. 0.017;
 Jones & Askew, LLP
191 Peachtree Street, 37th Floor
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/03757
FILING DATE: 29 SEPT 1994
ATTORNEY AGENT INFORMATION:
NAME: FROST, ROGER T.
REGISTRATION NUMBER: 22,176
REFERENCE/DOCKET NUMBER: 07826-0007
TELECOMONICATION INFORMATION:
TELECHONE: 404-818-3700
TELECHONE: 404-818-3700
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 US-08-817-547A-2; Sequence 2, Application US/08817547A; Patent No. 6030790; Fatent No. 6080780; GRNERAL INFORMATION:
 Sequence 1, Application US/08817547A Patent No. 6030790
 Query Match
Best Local Similarity 75.0%;
Matches 9; Conservative
 10 amino acids
 1 SVSEIQFMHNLG 12
 1 AVSEIQLXHNLG 12
 MOLECULE TYPE: peptide HYPOTHETICAL: no
 ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 1 SVSEIQFMHN 10
 SVSEIQLMHN 10
 unknown
 TYPE: amino acid
STRANDEDNESS: un
 Query Match
Best Local Similarity
Matches 9; Conserv
 CITY: Atlanta
STATE: Georgia
COUNTRY: USA
 ANTI-SENSE: no
US-08-817-547A-1
 TOPOLOGY:
 RESULT 2
US-08-817-547A-1
 STREET:
```

0

```
Sequence 10, Application US/09421379

Patent No. 649562

GENERAL INFORMATION:
APPLICANT: Gardella, Thomas J.
APPLICANT: Gardella, Thomas J.
APPLICANT: Potts, John T.
APPLICANT: Potts, John T.
APPLICANT: Potts, John T.
TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid;
TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid;
TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid;
TITLE OF INVENTION: Parathyroid Hormone, Related Peptide (PTHrP)

FILE REPERENCE: 0669.4570001

CURRENT FILING DATE: 1998-10-20

EARLIER APPLICATION NUMBER: U.S. 60/105,530

EARLIER PILING DATE: 1998-10-22

NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 10

LENGIN: DEA
 OTHER INFORMATION: Description of Artificial Sequence: synthetic proper INFORMATION: peptide US-09-421-379-10
 0
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 1; Indels
 47.5%; Score 29; DB 4; Length 9; 66.7%; Pred. No. 3e+05; 2; Indels native
 Score 31; DB 3;
Pred. No. 3e+05;
0; Mismatches
APPLICATION NUMBER: PCT/EPys, c...
FILING DATE: 29 SEPT 1994
ATTORNEY/AGENT INFORMATION:
NAME: FROST, ROGER T.
REGISTRATION NUMBER: 22,176
REGISTRATION NUMBER: 22,176
REFERENCE/DOCKET NUMBER: 07826-0007
TELEPANT 404-818-3700
TELEPANT 404-818-3790
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
LENGTH: design acids
 US-08-140-137A-42
; Sequence 42, Application US/08140137A
; Patent No. 5817617
; GENERAL INFORMATION:
APPLICANT: TUOMANEN, ELAINE
APPLICANT: MASURE, H. R.
 ORGANISM: Artificial Sequence FEATURE:
 Query Match
Best Local Similarity 87.5%;
Matches 7; Conservative
 SSS: unknown
unknown
 Conservative
 MOLECULE TYPE: peptide
 1 SVSEHOLLH 9
 1 SVSEIQFM 8
 HYPOTHETICAL:
 TOPOLOGY:
 US-08-817-547A-3
 US-09-421-379-10
 g
 .
0
 Gaps
 Sequence 7, Application US/09421379

Patent No. 6495662

GENERAL INFORMATION:
APPLICANT: Gardella, Thomas J.
APPLICANT: Forts, John T.
APPLICANT: Forts, John T.
APPLICANT: Ports, Harald
TITLE OF INVENTION: Boactive Peptides and Peptide Derivatives of
TITLE OF INVENTION: Boactive Peptides and Parathyroid
TITLE OF INVENTION: Hormone-Related Peptide (PTHYP)
TITLE OF INVENTION: Hormone-Related Peptide (PTHYP)
TITLE OF INVENTION: Hormone-Related Peptide (PTHYP)
TITLE NAME APPLICATION NUMBER: US 09/421,379
CURRENT FILING DATE: 1998-10-20

EARLIER APPLICANTON NUMBER: U.S. 60/105,530

EARLIER PILING DATE: 1998-10-22

NUMBER OF SEQ.ID NOS: 13

SOFURDARE: PatentIN Ver. 2.0
 OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: peptide
 .
0
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 1; Indels
 Query Match 54.1%; Score 33; DB 4; Length 9; Best Local Similarity 66.7%; Pred. No. 3e+05; Matches 6; Conservative 2; Mismatches 1; Indels
 Length 9;
 Sequence 3, Application US/08817547A
Patent No. 6030790
GENERAL INFORMATION:
APPLICANT: Adermann, Knut
APPLICANT: Hock, Dieter
APPLICANT: Magerlein, Markus
TITLE OF INVENTION: Peptides from the hPTH Sequence
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
'ADDRESSEE: Jones & Askew, LLP
 SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,547A
FILING DATE:
PRIOR APPLICATION DATA:
 Score 36; DB 4;
Pred. No. 3e+05;
1; Mismatches
 E: Jones & Askew, LLP
191 Peachtree Street, 37th Floor
 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
 STREET: 191 Peachtree Stree
CITY: Atlanta
STATE: Georgia
CCUNTRX: USA
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 TYPE: PRT
ORGANISM: Artificial Sequence
 Query Match
Best Local Similarity 77.6
Perina 7: Conservative
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1 AVSEIQLLH 9
 1 SVSEIQFMH 9
 1 AVSEIQLMH 9
 1 SVSEIQEMH 9
 US-09-421-379-7
 US-09-421-379-7
 δ
 g
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Gaps

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ö
 45.9%; Score 28; DB 6; Length 11; 60.0%; Pred. No. 32; 1; Mismatches 3; Indels
 47.5%; Score 29; DB 2; Length 12; 62.5%; Pred. No. 23;
 COUNTRY: USE.

ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DGS/MS-DGS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/140,137A
FILING DATE: Z7-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson EGQ., David A.
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 26,742
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
RELEFAX: 201 343-164
TELEFAX: 201 343-164
TELEFAX: 133521
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
FINGHH: 12 amino acids
FINGHH: 12 amino acids
 JACOPICAL ARTIN, THOMAS J.; MOSELEY, JANE M.; KEMP,
APPLICANT: MARTIN, THOMAS J.; MOSELEY, JANE M.; KEMP,
BRUCE E.; WETTENHALL, RICHARD E.H.
TITLE OF INVENTION: PROTEIN ACTIVE IN HUMORAL
HYPERCALCEMIA OF MALIGNANCY-PTHRP
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
PFLING DATE: 14-JUN-1991
PRIOR APPLICATION NUMBER: 199,235
FILING DATE: 09-MAY-1988
PRILING DATE: 09-MAY-1988
FILING DATE:
FILING DATE:
TITLE OF INVENTION: ANALOGS OF ENDOTHELIAL LEUKOCYTE
TITLE OF INVENTION: ADHESION MOLECULE (ELAM)
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
 MOLECULE TYPE: peptide
; DESCRIPTION: CaRD peptide segence
US-08-140-137A-42
 Query Match
Best Local Similarity 60.0.
 5; Conservative
 STREET: 411 Hackens
CITY: Hackensack
STATE: New Jersey
 5 ISEEQFVH 12
 Best Local Similarity
Matches 5; Conserva
 2 VSEIQFMH 9
 LENGTH: 11
 Query Match
 SEQ ID NO:3:
 5460978-3
 5460978-3
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 Gaps
 Length 6;
 CONDUCES: Jones & Askew, LLP
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: 6Goorgia
COUNTRY: USA
ZIP: 30303
COMPUTER READELE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC Compatible
OPERATING SYSTEM: PC-DOS/NM-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,547A
 APPLICANT: Adermann, Knut
APPLICANT: Adermann, Knut
APPLICANT: Hock, Dieter
APPLICANT: Magellein, Markus
TITLE OF INVENTION: Peptides from the hPTH Sequence
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSE: Jones & Askew, LLP
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
 GENERAL INFORMATION:
APPLICANT: Adermann, Knut
APPLICANT: Hock, Dieter
APPLICANT: Magellein, Markus
TITLE OF INVENTION: Peptides from the hPTH Sequence
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew, LLP
 42.6%; Score 26; DB 3;
100.0%; Pred. No. 3e+05;
 100.0%; Pred. No. ...
 FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/03757
APPLICATION NUMBER: 29 SEPT 1994
ATTORNEY/AGENT INFORMATION:
NAME: FROST, ROGERT.
RESISTRATION NUMBER: 22.176
REFERENCE/DOCKET NUMBER: 07826-0007
 07826-0007
 Sequence 4, Application US/08817547A Patent No. 6030790 GENERAL INFORMATION:
; Sequence 5, Application US/08817547A; Patent No. 6030790
 TELEPRONE 404-818-3700
TELEPRONE 404-818-3700
TELEPRONE 404-818-3799
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
 Best Local Similarity 100.
Matches 6; Conservative
 TOPOLOGY: unknown
MOLECULE TYPE: peptide
 TYPE: amino acid
STRANDEDNESS: unl
 1 SVSEIQ 6
 ; ANTI-SENSE: no
US-08-817-547A-5
 STATE: G
 US-08-817-547A-4
 LENGTH:
 Query Match
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SSVTFMH 11
 3 SEIQFMH 9
 US-08-482-228-42
 TOPOLOGY:
 US-08-482-528-42
 RESULT 14
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 Gaps
 Gaps
 Sequence 8, Application US/09421379;
Parent No. 649562
Sequence 8, Application US/09421379;
Parent No. 649562
Sequence 8, Application US/09421379;
Parent No. 649562
Sequence 8, Application:
Sequence 8, Application:
Sequence 8, Application:
Sequence 8, Application:
Septide Norman Sequence 8, Application Norman Trille OF INVENTION:
Parenthyroid Hormone-Related Peptide (PTH) and Parathyroid
TITLE OF INVENTION: Parathyroid Hormone-Related Peptide (PTHP)
TITLE OF INVENTION: Parathyroid Hormone-Related Peptide (PTHP)
TITLE OF INVENTION: 1999-10-20
CURRENT APPLICATION NUMBER: US. 60/105,530
EARLIER PILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 8
LENGTH: 9
 OTHER INFORMATION: Description of Artificial Sequence: synthetic; OTHER INFORMATION: peptide US-09-421-379-8
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0
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 0; Indels
 DB 3; Length 7; 3e+05;
 Query Match 42.6%; Score 26; DB 4; Length 9; Best Local Similarity 55.6%; Pred. No. 3e+05; Matches 5; Conservative 2; Mismatches 2; Indels
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,547A
FILING DATE: 29 SEPT 1994
ATYONEY/AGENT INPORMATION:
NAME: PROST ROCER T.
REGISTRATION NUMBER: 22,176
REGISTRATION NUMBER: 22,176
REGISTRATION INFORMATION:
TELEPHONE: 404-818-3700
TELEPHONE: 404-818-3700
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LEMEGRIF: 7 amino acids
LEMEGRIF: 7 amino acids
 Query Match 42.6%; Score 26; DB Best Local Similarity 100.0%; Pred. No. 3e+Matches 6; Conservative 0; Mismatches
 TYPE: PRT
ORGANISM: Artificial Sequence
 TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
 MOLECULE TYPE: peptide HYPOTHETICAL: no
 :||| | :|
1 AVSEHQLLH 9
 1 SVSEIQFMH 9
 1 SVSEIQ 6
 |||||||
1 SVSEIQ 6
 ; ANTI-SENSE;
US-08-817-547A-4
 RESULT 12
US-09-421-379-8
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-177-109A-56
Query Match
Best Local Similarity 60.0%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 8 MHNLG 12
Cy 8 MHNLG 12
Db 1 LHNMG 5
Search completed: September 5, 2004, 09:38:33
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|               | Ltd.               |
|---------------|--------------------|
| 5.1.6         | Compugen           |
| version 5.1.6 | - 2004             |
| GenCore       | Copyright (c) 1993 |
|               |                    |

OM protein - protein search, using sw model

5, 2004, 09:30:43; Search time 9.5 Seconds (without alignments) 121.505 Million cell updates/sec Title:

September

Run on:

US-09-730-174A-5 59 Perfect score:

1 AVSEIQLMHNLG 12 Scoring table: Sequence:

283366 segs, 96191526 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

1581 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 12

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

|   |        | Description | heavy | arnocin UI49 - C | Ч  | sperm-activating p | lgen p20e pr | oimidazole | sin heav | g heavy chain | -cell receptor a | -cell receptor | -cell receptor | cental lactod | •    | pilE protein - Esc | polyphosphate-qluc | chlorophyll a/b-bi | N-methylpurine DNA | T-cell receptor da | Ω    | translation elonga | in   | COI intron 16 prot | ö    | Id heavy chain CRD | uromedin K - pi |      | al prot | nin C | amine oxidase (cop |
|---|--------|-------------|-------|------------------|----|--------------------|--------------|------------|----------|---------------|------------------|----------------|----------------|---------------|------|--------------------|--------------------|--------------------|--------------------|--------------------|------|--------------------|------|--------------------|------|--------------------|-----------------|------|---------|-------|--------------------|
|   |        |             | 0     | Н                | N  | α                  | S            | $\epsilon$ | Ø        | ø             | ω,               | α              | $\infty$       | ω             | N    | 9                  | 3                  | 002                | 2                  | 33                 | 4    | 3                  | g    | œ                  | Т    | m                  | INK             | 155  | 173     | 1033  | 04                 |
|   |        | OI :        |       | A587             | œ  | A605               | B464         | A558       | I468     | ~             | PH11             | PH11           | PH11           | A473          | PH09 | S252               | S297               | PWOO               | A560               | E490               | A388 | B418               | A407 | m                  | T095 | 0                  | SPPG            | 8280 | S278    | C610  | 8713               |
|   | 8      | 8           | 7     | 7                | C) | N                  | C)           | ~          | (A)      | N             | C3               | 7              | 7              | N             | Ŋ    | N                  | Ŋ                  | N                  | N                  | N                  | (7   | N                  | 7    | 0                  | N    | ~                  | Н               | N    | 7       | 7     | 71                 |
|   |        | Length      | 12    | 7                | 6  | 10                 | 10           | 12         | 7        | 10            | 12               | 12             | 12             | 10            | 11   | 7                  | 7                  | σ                  | ტ                  | 10                 |      | 11                 |      | 4                  | 7    | σ                  | 10              | 10   | 10      | 10    | 11                 |
| ₩ | Query  | Match       | •     | •                |    |                    |              |            |          |               |                  |                |                | •             | 27.1 |                    | 25.4               | 25.4               | 25.4               | 25.4               | 25.4 | 25.4               |      |                    |      |                    | 23.7            |      |         | 23.7  | 23.7               |
|   |        | score       |       |                  |    |                    |              |            |          |               |                  |                |                |               |      |                    |                    |                    |                    | 15                 |      |                    |      |                    |      |                    |                 |      |         |       |                    |
|   | Result | NO.         | н     | 7                | m  | 4                  | ហ            | w          | 7        | ထ             | σ                | 10             | 11             | 12            | 13   | 14                 |                    |                    |                    | 18                 |      |                    |      |                    |      |                    |                 |      |         |       |                    |

| retinal oxidase -<br>acidic proline-ric<br>hypothetical profe | transcription fact<br>t-complex polypept<br>potB protein - Sal | T-cell receptor al<br>T-cell receptor al<br>glutamine tRNA lig | anglotensin-conver<br>hypothetical prote<br>leucokinin VI - Ma<br>IO H chain V-D-J r | coat protein beta<br>sperm-activating p<br>Ig heavy chain CDR |
|---------------------------------------------------------------|----------------------------------------------------------------|----------------------------------------------------------------|--------------------------------------------------------------------------------------|---------------------------------------------------------------|
| 1 2 S60354<br>1 2 B29806<br>1 4 S41909                        | 2 2 S25485<br>2 2 G49410<br>2 2 S71034                         | 2 2 PH1175<br>2 2 PH1174<br>2 2 141235                         | 5 7 14906<br>8 2 114906<br>8 2 050316<br>8 2 PH1618                                  | 9 2 S13636<br>9 2 JN0026<br>9 2 PT0231                        |
| 14 23.7 1                                                     | 14 23.7 1                                                      | 14 23.7 1                                                      | 13 22.0                                                                              | 13 22.0                                                       |
| 14 23.7 1                                                     | 14 23.7 1                                                      | 14 23.7 1                                                      | 13 22.0                                                                              | 13 22.0                                                       |
| 14 23.7 1                                                     | 14 23.7 1                                                      | 14 23.7 1                                                      | 13 22.0                                                                              | 13 22.0                                                       |
| 30                                                            | . u w w e                                                      | 9 F 80 C                                                       | 21 44 44                                                                             | 4 4 4                                                         |
| 32                                                            | w 44 70 2                                                      |                                                                | 22 0 14 64                                                                           | ይ 4 7                                                         |

S21205

S21205

Garles and Varedon - human

C.Species: Homo sapiens (man)

C.Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 16-Aug-1996

C.Accession: S21205

R.Makiya, R.; Stigbrand, T.

Eur. J. Biochem. 205, 341-345, 1992

R.Makiya, R.; Stigbrand, T.

Eur. Sight and Sallos phosphatase has a binding site for the human immunoglobulin. A.Reference number: S21205; MUID:92209522; PMID:1555592

A.Accession: S21205

A.Accession: S21205

A.Accession: preliminary

A.Molecule type: protein

A.Residues: 1-12 < MAK>

C.Keywords: heterotetramer; immunoglobulin

ö Gaps 0 Query Match 35.6%; Score 21; DB 2; Length 12; Best Local Similarity 44.4%; Pred. No. 6.9e+02; Matches 4; Conservative 3; Mismatches 2; Indels

4 EIQLMHNLG 12 

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Carnocin UI49 - Carnobacterium sp. (fragment)
C.Species: Carnobacterium sp.
C.Species: Carnobacterium sp.
C.Date: 23-Jan-1998 #sequence\_revision 30-Jan-1998 #text\_change 30-Jan-1998
C.Accession: A58718
R.Stoffels, G.; Nissen-Meyer, J.; Gudmundsdottir, A.; Sletten, K.; Holo, H.; Nes, I.F.
Appl. Environ. Microbiol. 58, 147-1422, 1992
A.Title: Purification and characterization of a new bacteriocin isolated from a Carnobac

A,Accession: A58718
A,Status: preliminary
A,Molecule type: protein
C,Keywords: 1-7 <STO>

. 0 Query Match 30.5%; Score 18; DB 2; Length 7; Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 4; Conservative 0; Mismatches 0; Indels

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Gaps

3 SEIQ 6 SEIO 5 ~ d ð

RESULT 3 S78420

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no.coc

C,Species: Mus musculus (house mouse)

C,Species: Mus musculus (house mouse)

C,Date: 19-Mar-1997 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998 °

C,Accession: A37268

R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.

A; Baol. Chem. 266, 6607-6613, 1991

A;Title: Heavy and light chain variable region sequences and antibody properties of anti-

A;Reference number: A38740; MUID:91177923; PMID:1706720
 alpha-myosin heavy chain - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 05-Nov-1999
C;Accession: 146868
R;Friedman, D.J.; Umeda, P.K.; Sinha, A.M.; Hsu, H.
R;Friedman, D.J.; Umeda, P.K.; Sinha, A.M.; Hsu, H.
A;Tritle: Characterization of genomic colones specifying rabbit alpha- and beta-ventricula
A;Reference number: 146868; MUID:84221901; PMID:6328491
 5-aminoimidazole ribonucleotide carboxylase/4-N-succinylamino carbonyl-5-aminoimidazole C;Species: Gallus gallus (chicken)
C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 17-Mar-1999
C;Datesion: ASSAD Bayusson, V.J.
B;Accession: ASSAD Davisson, V.J.
Biochemistry 33, 11917-11926, 1994
A;Ritle: Carboxylases in de Novo purine biosynthesis. Characterization of the Gallus gall A;Reference number: ASSB37; MUID:95001903; PMID:7918410
 A; Cross-references: GB: K01698; NID: 9165538; PIDN: AAA31415.1; PID: 9165539
 Score 17; DB 2; Length 10;
Pred. No. 3.3e+03;
1; Mismatches 4; Indels
 Score 18; DB 2; Length 12;
Pred. No. 2.6e+03;
 1; Indels
 2; Indels
 Score 17; DB 2; Length 7; Pred. No. 2.8e+05; 1; Mismatches 1; Indels
 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-7 <FRI>
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 28.8%;
 Query Match 28.8%;
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Matches 3; Conservative
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Best Local Similarity 57.1%;
Matches 4; Conservative
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 A,Status: preliminary
A,Molecule type: protein
A,Residues: 1-12 <FIR>
 1 AVSEIQL 7
 2 AASELAL 8
 OLMHN 10
 A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-10 <RUF>
 OKMHD 5
 :|| |
1 MOLFH 9
 A;Accession: 146868
 A; Accession: A37268
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 e antigen p20e precursor - hepatitis B virus (subtype adr) (fragment)
NyAlternate names: HBe antigen precursor
NyAlternate names: HBe antigen precursor
C.Species: hepatitis B virus, HBV
A.Variety: subtype adr
C.Species: hepatitis B virus, HBV
C.Accession: B46453
R.Takahashi, K.; Kishimoto, S.; Ohori, K.; Yoshizawa, H.; Machida, A.; Ohnuma, H.; Tsuda
A.Title: Molecular heterogeneity of e antigen polypeptides in sera from carriers of hepatines on the control of the con
 sperm-activating peptide (Tyr-2, Asn-3, Gly-5, Ile-9, Asp-10 SAP-1) - slate-pencil urchi
C;Species: Heterocentrotus mamillatus
C;Date: 17-Apr-1933 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
C;Accession: A60589
R;Yoshino, K.I.; Kajiura, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamagud
Comp. Biochem. Physiol. B 94, 739-751, 1989
A;Title: A halogenated amino acid-containing sperm activating peptide and its related pe
otus nudus, Echinometra mathaei and Heterocentrotus mammillatus.
 ..
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ribosomal protein RL41, mitochondrial [validated] - rat (fragment)
C,Species: Rattus norvegicus (Norway rat)
C,Bate: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jul-2000
C,Accession: S74420
R;Goldschmidt-Reisin, S.; Graack, H.R.
submitted to the Protein Sequence Database, February 1998
A,Refession: S7841
A,Refession: S78420
A,Molecule type: protein
A,Residues: 1-9 <GD.
A,Molecule type: protein
A,Residues: 1-9 <GD.
C,Keywords: mitochondrion; protein biosynthesis; ribosome
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 A,Status: preliminary
A,Molecule type: protein
A,Residues: 1-10 ~TAK>
A,Experimental source: subtype adr
A,Experimental source: subtype adr
A,Note: sequence extracted from NCBI backbone (NCBIP:60243)
F,1-10/Domain: signal sequence (fragment) #status predicted <SIG>
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 1; Indels
 Length 9;
 Query Match
30.5%; Score 18; DB 2; I
Best Local Similarity 60.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 1; Mismatches 1;
 Score 18; DB 2; I
Pred. No. 2.8e+05;
0; Mismatches 1;
 A, Accession: A60589
A, Molecule type: protein
A, Residues: 1-10 <705>
C, Superfamily: unassigned animal peptides
 30.5%;
 Query Match
Best Local Similarity 75.v.
3; Conservative
 3; Conservative
 Query Match
Best Local Similarity
 :|||
YNLG 5
 9 HNLG 12
 9 HNLG 12
 HRLG 8
 A; Accession: B46453
 Matches
 Db
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pilE protein - Escherichia coli (fragment)
C;Species: Escherichia coli
C;Species: Escherichia soli
C;Species: Escherichia soli
C;Species: S52266
R;Dupuy, B.; Taha, M.K.; Possot, O.; Marchal, C.; Pugsley, A.P.
Mol. Microbiol. 6, 1887-1894, 1992
A;Title: PulO, a component of the pullulanase secretion pathway of Klebsiella oxytoca, characteric muchaer: S25266, MUID:92374839; PMID:1354833
A;Accession: S25266
A;Accession: S25266
A;Accession: C;Genetics:
A;Genetics:
A;Genetics:
 C;Species: Mus sp. (mouse)
C;Species: Mus sp. (mouse)
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 12-Aug-1996
C;Accession: A47364 #sequence_revision 12-Aug-1996 #text_change 12-Aug-1996
C;Accession: A47364 #sequence_revision 12-Aug-1996 #text_change 12-Aug-1996
B;Shida, M. M.; Mg, Y. K.; Soares, M.J.; Linzer, D.I.
Mol. Endocrinol. 7, 181-188, 1993
A;Title: Trophoblast-specific transcription from the mouse placental lactogen-I gene pr A;Accession: A47364 MUD:93225959; PMID:8469232
A;Accession: A47364
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Kesidues: 1-10 <RES>
A;Cross-references: GB:S58124; NID:g299449
 T-cell receptor beta chain V-D-J region (isolate 10) - rat (fragment)
C;Species: Rattus norregicus (Norway rat)
C;Species: Rattus norregicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0924
R;Gold, D.P.; Offiner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allerg A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0924
A;Accession: PH0924
A;Molecule type: mRNA
A;Residues: 1-11 <GOL>
A;Residues: 1-11 <GOL>
A;Residues: 1-11 <GOL>
A;Residues: T-cell receptor
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 Length 10;
 Length 11;
 2; Indels
 Query Match 25.4%; Score 15; DB 2; Length 7; Best Local Similarity 75.0%; Pred. No. 2.8e+05; Matches 3; Conservative 1; Mismatches 0; Indels
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 27.1%; Score 16; DB 2; I 50.0%; Pred. No. 5.7e+03; tive 1; Mismatches 3;
 placental lactogen-I precursor - mouse (fragment)
 Query Match
Best Local Similarity 50.0
Matches 4; Conservative
 5 IQLMHNL 11
 2 ASSSMDLM 9
 1 MOLTLNL 7
 1 AVSEIQLM
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 T-cell receptor alpha chain V region (Cw3/10.1) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 16-Unl-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C;Accession: PH1190
R;Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid A;Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor A;Reference number: S26512; MulD:92364546; PMID:1380061
A;Accession: PH1190
A;Accession: PH1190
A;Accession: PH1190
A;Accession: PH1190
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C;Accession: PH189
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C;Date: 16-Ju1-1999 #sequence_revision 16-Ju1-1999 #text_change 16-Ju1-1999
C;Accession: PH187
R;Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid A;Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor A;Reference number: S26512; MUID:92364546; PMID:1380061
A;Accession: PH1187
A;Accession: PH1187
A;Accession: preliminary
A;Molecule type: mRNA
A;Residues: 1-12 cCAS>
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 Query Match

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Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels
 28.8%; Score 17; DB 2; Length 12;
llarity 100.0%; Pred. No. 4e+03;
Conservative 0; Mismatches 0; Indels
 Query Match 28.8%; Score 17; DB 2; Length 12; Best Local Similarity 100.0%; Pred. No. 4e+03; Matches 4; Conservative 0; Mismatches 0; Indels
| | | | | 1 | 1 | 1 | ESQSFPNVG 9
 Query Match
Best Local Similarity
Matches 4; Conserv
 1 AVSE 4
 AVSE 5
 2 AVSE 5
 1 AVSE 4
 RESULT 11
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RESULT 15
S29735
Clothorsphate-glucose phosphotransferase (EC 2.7.1.63) - Propionibacterium freudenreichi Cjoptonibacterium freudenreichi subsp. shermanii
Cjobte: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 03-Jun-2002
Cjocesalon: S29735
R.Phillips, N.F.B.; Horn, P.J.; Wood, H.G.
Arch. Biochem. Blophys. 300, 309-319, 1993
A.Title: The polyphosphate- and ATP-dependent glucokinase from Propionibacterium sherman A.Reference number: S29735; MUD:93143332; PMID:8380966
A.Status: preliminary
A.Status: preliminary
A.Status: preliminary
A.Status: Propionibacterium sherman A.Status: Propionibacter
5 IQLM 8
|:||
4 IELM 7
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Gaps ; 0 Query Match 25.4%; Score 15; DB 2; Length 7; Best Local Similarity 75.0%; Pred. No. 2.8e+05; Matches 3; Conservative 0; Mismatches 1; Indels

0

9 HNLG 12

ð g

2 HVLG 5

Search completed: September 5, 2004, 09:37:44 Job time : 9.5 secs

OM protein - protein search, using sw model

September 5, 2004, 09:27:07; Search time 6.5 Seconds (without alignments) 96.130 Million cell updates/sec Run on:

US-09-730-174A-5 59

1 AVSEIQLMHNLG 12 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 segs, 52070155 residues Searched:

501 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 12

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt 42:\* Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Description                  |            | 20   | 0 clostridi | 7          | 4          | 8          | Ħ          | 2          | H          | 0          | 2          |           | m          | 0 rana     | ď        | 9          | 'n         | ø          | 3 methanob | d          | 3 leucophae | 8          | N  | 1 periplane | ø  |            | 4 comamonas | 0 peripl   | 3 papio he | '5 litoria | 8 homo | 49 clupea  |
|------------------------------|------------|------|-------------|------------|------------|------------|------------|------------|------------|------------|------------|-----------|------------|------------|----------|------------|------------|------------|------------|------------|-------------|------------|----|-------------|----|------------|-------------|------------|------------|------------|--------|------------|
|                              | 1          |      |             |            |            |            |            |            |            |            |            |           |            |            |          |            |            |            |            |            |             |            |    |             |    |            |             |            |            |            |        |            |
| d D                          | LANC CARUI | - 1  |             | PVK1_PERAM | TRPI_PSEPU | ALL7_CYDPO | AL18_CARMA | ALL1_CYDPO | FAR8_MACRS | UF02_MOUSE | AL19_CARMA | SBF_CAPAN | TEMK_RANTE | TKNC_RANCA | TKNK_PIG | ASL1_BACSE | CD11_LITXA | CD14_LITXA | PORD_METTM | RS19_TOBBP | LCK4_LEUMA  | LCK6_LEUMA |    | PPK1_PERAM  | 4  | CSI5_BACSU | 1           | PPK4_PERFU | 133        | - 1        | MEI    | GON1_CLUPA |
| DB 1                         |            |      |             |            |            |            |            |            |            |            |            |           |            |            |          |            | 7          |            |            |            |             |            |    |             |    |            |             |            |            |            |        | о<br>Н     |
| %<br>Query<br>Match Length I |            | 0 00 | 11          | 11         | <b>Q</b>   | 7          | Φ.         | ω .        | σ.         | σ          | 10         | 10        | 10         | 10         | 10       | 11         | 12         | 12         | 12         | 12         | œ           | <b>c</b> o | თ  | თ           | 10 | 11         | 11          | 12         | σı         |            | 10     |            |
| %<br>Query<br>Match          | 30.5       |      | 7.          | 25.4       | 23.7       | 23.7       | 23.7       | m,         | 23.7       | m          | M          | m<br>m    | 23.7       | ო          | m<br>m   | ო          | 23.7       | m          | ۳.         | ო          | Α.          | ď.         | 2  | ď.          | ď. | 'n         | 'n          | ď.         |            | 0          | 0      |            |
| Score                        | 18         | 16   | 16          | 15         | 4          | 14         | 14         | 14         | 14         | 14         | 14         | 14        | 14         | 14         | 14       | 14         | 14         | 14         | 14         | 14         | 13          | 13         | 13 | 13          | 13 | 13         | 13          | 13         | 12         | 12         | 12     | 12         |
| Result<br>No.                |            | ۱m   | 41          | <u>س</u>   | <b>1</b> W | ۲ (        | ao (       | on (       | 0 1        | 11         | 12         | 13        | 14         | 15         | 16       | 17         | 18         | 19         | 20         | 21         | 22          | 23         | 24 | 25          | 26 | 27         | 28          | 50         | 30         | H (        | 3.5    | en<br>en   |

| P80678 chelyosoma P18110 romalea mic P18135 hellothis z Q46464 campylobact P29135 rana ridibut P58807 comus marmo P81672 pinus pinas P31031 proteus vul P83654 bacceroides P82065 litoria rub P81675 pinus pinas P81675 pinus pinas |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| GONZ CHEPR<br>HTF1_ROMMI<br>HTF ELZE<br>SYK GANUP<br>CXAL CONNR<br>CXAL CONNR<br>HSP1_PROVU<br>HSP1_PROVU<br>HSP1_BACSE<br>PR4 PERAM<br>TY51_LITRU<br>UNO6_PINPS                                                                    |
| ееналапалапа                                                                                                                                                                                                                        |
| 100<br>100<br>100<br>100<br>100<br>100<br>100<br>100<br>100<br>100                                                                                                                                                                  |
| 66 W W W W W W W W W W W W W W W W W W                                                                                                                                                                                              |
|                                                                                                                                                                                                                                     |
| w w w w w w a a a a a a a<br>a n n n c m n o c m o c m o c a n                                                                                                                                                                      |

#### ALIGNMENTS

RESULT 1

| LANC_CARUI  IDANC_CARUI  IDANC_ | PANDARD; PRT; 7 AA.  29, Created)  29, Last sequence update)  29, Last sequence.  29, Last sequence.  29, Last sequence.  20, Last sequence.  30, Strain U149)  20, Strain U149)  30, Strain U149)  31, Length 7;  31, Strain U149)  32, Strain U149)  33, Strain U149)  34, Strain U149)  35, Strain U149)  36, Strain U149)  37, Strain U149)  38, Strain U149)  39, Strain U149)  30, Strain U149)  31, Length 7;  31, Tantibiotic. |
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ALLG CYDPO STANDARD; PRT; 8 AA.

PB2157;

90-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
Cydiastatin 6.

Cydiastatin (Codling moth).

Cydia pomonella (Codling moth).

Staryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neottera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Tortricoidae; Tortricidae; Olethreutinae; Cydia. ALL6 CYDPO
ID ALL6 CYDPO
DT 30-MAY
DT 30-MAY
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DE CYGIA:
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RY MEDUVE H
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RA DAVEY
RT "LEPIG RESULT 2

SEQUENCE.
TISSUB-Larva;
MISCALINE-98054539; PubMed-9392829;
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D., Davey M., East P.D., Thorpe A.;
"Lepidopteran peptides of the allatostatin superfamily.";
Peptides 18:1301-1309(1997).

11.

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5 IQLMHNLG
 NCBI_TaxID=303;
 Pseudomonas
 PVKI PERAM P41837;
 PSEPU
 SEQUENCE
 Query Match
 putida.
 RESULT 6
TRPI_PSEPU
 P36414
 PVK1_PERAM
 Best Loc
Matches
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 Flengsrud R., Skjeldal L., "Two-dimensional Belectrophoresis separation and N-terminal sequence analysis of proteins from Clostridium pasteurianum W5."; Blectrophoresis 19:802-806 (1998).

--- FUNCTION: This protein promotes the GTP-dependent translocation of the nascent protein chain from the A-site to the P-site of the
 Gaps
 Gaps
 -!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
EF-G/EF-2 subfamily.
InterPro; IPR000795; EF-GTPbind.
 Clostridium pasteurianum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
NCBI_TaxID=1501;
 .
0
 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Allergen Fus s 13596* (Fragment).
Fusarium solani (subsp. pisi) (Nectria haematococca).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
 .
0
 Score 16; DB 1; Length 8; Pred. No. 1.4e+05; 2; Mismatches 1; Indels
 Length 8;
 1; Indels
 STRAIN=TARI 3596; TISSUB=Mycellum;
Verma J., Gangal S.V.;
Submitted (JUL-1997) to Swiss-Prot.
-!- ALLERGEN: Causes an allergic reaction in human.
Allergen.
 8 8 AA; 898 MW; C372C441F5B69041 CRC64;
 -!- SIMILARITY: Belongs to the allatostatin family
 AMIDATION.
0B2879C45B573767 CRC64;
 Score 16; DB 1; Dred. No. 1.4e+05; 2; Mismatches 1
 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-BEB-2003 (Rel. 41, Last annotation update)
Blongation factor G (EF-G) (CP 5) (Fragment).
 B AA.
 11 AA
 MEDLINE=98291870; PubMed=9629918;
 27.18;
40.08;
 27.18;
40.08;
 8 AA; 936 MW;
 Local Similarity 40.0
les 2, Conservative
 Neuropeptide, Amidation.
MOD RES 8 8
SEQUENCE 8 AA; 936 MW;
 2; Conservative
 STANDARD;
 STANDARD;
 Query Match
Best Local Similarity
 8 MHNLG 12
 LMHNL 11
 LYNFG 7
 MSHNV 7
 FUSSO
 STRAIN=W5;
 CLOPA
 NON TER
SEQUENCE
 SEQUENCE
 Query Match
 FUSS FUS
 RESULT 3
FUSS FUSSO
 Matches
 RESULT
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 01-UTN-1994 (Rel. 29, Created)
01-UTN-1994 (Rel. 29, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
HTH-type transcriptional regulator trpl (TrpBA operon transcriptional activator) (Fragment).
 TISSUBACE, AND SYNTHESIS.

TISSUB-Abdominal perisympathetic organs;

MEDINE-9523021; PubMed=7716075;

MEDINE-9523021; PubMed=7716075;

"Perintne-9523021; PubMed=7716075;

"Perintne-9523021; PubMed=7716075;

"Perintne-9523021; PubMed=7716075;

"Perintne-9523021; PubMed=77195;

"Perintne-9523021;

"Perintne
 Gaps
 Bicchimie 71:521-531(1989).
-!- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPBA GENES ENCODING
 Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
Pseudomonadaceae, Pseudomonas.
 .
0
 .
0
 Periplaneta americana (American cockroach).
Eukaryota, Metazoa, Arthropoda; Hexapoda, Insecta, Pterygota,
Neoptera; Orthopteroidea, Dictyoptera, Blattaria, Blattoidea,
 Bberly L., Crawford I.P.;
"DNA sequence of the tryptophan synthase genes of Pseudomonas
 Score 15, DB 1, Length 11;
Pred. No. 5.5e+03;
1; Mismatches 2; Indels
 Length 11;
 3; Indels
PROSITE; PS00301; BFACTOR GTP; PARTIAL.
Elongation factor; Protein biosynthesis; GTP-binding.
NON TER 11 11
SEQÜENCE 11 AA; 1337 MW; 412E71F1D9C33B17 CRC64;
 AMIDATION.
39DB5419D7605728 CRC64;
 Score 16; DB 1; I
Pred. No. 3.5e+03;
3; Mismatches 3;
 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Periviscerokinin-1 (Pea-PVK-1).
 11 AA
 6 AA
 STRAIN=PPG1 C1S;
MEDLINE=89335826; PubMed=2503057;
 27.1%;
25.0%;
 25.4%;
 11 AA; 1114 MW;
 Neuropeptide; Amidation.
MOD RES 11 11
 Conservative
 STANDARD;
 STANDARD;
 Blattidae; Periplaneta.
NCBI_TaxID=6978;
 12
 4 LEKFÖNIG 11
 SEQUENCE FROM N.A.
 5 IQLMHN 10
 Local Similarity
les 2; Conserv
```

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"Isolation and identification of multiple neuropeptides of the allatostatin superfamily in the shore crab Carcinus maenas."; bur. U. Biochem. 250:727-34(1997).

-!- FUNCTION: May act as neurotransmitter or neuromodulator.

-!- SIMILARITY: Belongs to the allatostatin family.

Neuropeptide; Amidation; Multigene family.

MOD RES 8

AMIDATION (POTENTIAL).

SEQUENCE 8 AA; 919 MW; C82879D5ABS5G9ABS CRC64;
 Cydia pomonella (Codling moth).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neophera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Tortricoidea; Tortricidae; Olethreutinae; Cydia.
 Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 Carcinus maenas (Common shore crab) (Green crab).

Metazoa; Arthropoda; Crustacea; Malacostraca;

Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;

Bubrachyura; Portunoidea; Portunidae; Carcinus.
 23.7%; Score 14; DB 1; Length 8; 40.0%; Pred. No. 1.46+05; Attive 2; Mismatches 1; Indels
 Query Match 23.7%; Score 14; DB 1; Length 8; Best Local Similarity 50.0%; Pred. No. 1.4e+05; Matches 2; Conservative 1; Mismatches 1; Indels
 P83281,
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
FMRFamide-like neuropeptide FLPB (VSHNFLRF-amide).
Macrobrachium rosenbergii (Giant fresh water prawn)
 8 AA; 934 MW; C82879C45B51F775 CRC64;
 TISSUE-Cerebral ganglion, and Thoracic ganglion; MEDLINE-98121193; PubMed-9461295;
 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Cydiastatin 1.
 8 AA.
 9 AA.
 PRT;
 Conservative
 Neuropeptide, Amidation.
MOD_RES 8 8
SEQUENCE 8 AA; 934 MW.
 STANDARD;
 STANDARD;
 Query Match
Best Local Similarity
2, Conserva
 8 MHNLG 12
 3 MYSFG 7
 9 HNLG 12
 4 YNFG 7
 ALL1 CYDPO
P82152;
 FARB MACRS
 Thorpe A.,
 SECUENCE
 RESULT 9
ALL1 CYDPO
 OFF
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THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE INDUCER (INDOLEGIZCEROL PROSPHATE), TRYPT BINDS UPSTREAM OF THE TRAB OPERON, OVERLAPPING ITS OWN PROMOTER REGION. SIMILARITY: Contains 1 HTH lysR-type DNA-binding domain.
 Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D., Davey M., East P.D., Thorpe A.;

"Leptdopteran peptides of the allatostatin superfamily.";

Peptides 18:1301-1309(1997).

- I SIMILARITY: Belongs to the allatostatin family.

Neuropeptide; Amidation.

AMIDATION.
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 Eŭkaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Lepidoptera, Glossata, Ditrysia, Tortricoidea, Tortricoidea, Olethreutinae, Cydia.
 Tryptophan biosynthesis; Transcription regulation; Activator; DNA-binding.
 23.7%; Score 14; DB 1; Length 6; 40.0%; Pred. No. 1.4e+05; tive 2; Mismatches 1; Indels
 23.7%; Score 14; DB 1; Length 7; 40.0%; Pred. No. 1.4e+05;
 1; Indels
 NON TER 6 6
SEQUENCE 6 AA; 683 MW; 77672AA1EDD6F000 CRC64;
 7 7 AMIDATION.
7 AA; 873 MW; 672879CABB569350 CRC64;
 30-MAY_2000 (Rel. 39, Created)
30-MAY_2000 (Rel. 39, Last sequence update)
30-MAY_2000 (Rel. 39, Last annotation update)
 Last sequence update)
Last annotation update)
 7 AA.
 8 AA.
 2; Mismatches
 Interpro; IPR000847; HTH LYSR.
PROSITE; PS50931; HTH LYSR; PARTIAL.
 TISSUE=Larva;
MEDLINE=98054539; PubMed=9392829;
 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last seq.
30-MAY-2000 (Rel. 39, Last anno
 EMBL; X13299; CAA31660.1; -.
 Query Match
Best Local Similarity 40.0
Matches 2; Conservative
 STANDARD;
 Local Similarity 40.0
 STANDARD;
 7 LMHNL 11
 8 MHNLG 12
 |:: |
2 MYDFG 6
 1 MAHDL 5
 Carcinustatin 18.
 Cydiastatin 7.
 AL18_CARMA
P81821;
 CYDPO
 SEQUENCE
 SEQUENCE
 Query Match
 ALL7 CYD
P82158;
 RESULT 7
ALL7_CYDPO
 AL18 CARMA
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RESULT 8

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 Entarycta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Capsicum.
 HAMAP; MF 00643; -; 1.
InterPro; IPR006216; Cyt_b559.
PR05ITE; PS00537; CYTOCHROME_B559; PARTIAL.
CCHOroplast; Photosystem II; Heme; Electron transport; Transmembrane.
NON_TER
 01-JTN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Cytochrome bS59 beta subunit (PSII reaction center subunit VI)
 Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae; Carcinus.
 Score 14; DB 1; Length 10;
Pred. No. 7.7e+03;
2; Mismatches 1; Indels
 TIŜSUE-Cerebral ganglion, and Thoracic ganglion;
MEDLINE-98121193; PubMed-9461295;
 Capsicum annuum (Bell pepper).
Chloroplast.
 23.7%;
 EMBL; X65570; CAA46539.1; -. PIR; S28055; S28055.
 2; Conservative
 Local Similarity
 8 MHNLG 12
 |:: |
5 MYSFG 9
 lamiids; Solanale
NCBI_TaxID=4072;
 (Fragment).
 PSBF_CAPAN
Q03367;
 SEQUENCE
 Query Match
 PSBE_CAPAN
 RESULT 13
 SET THE SET OF S
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 TISSUE=Fibroblast,
MEDIINE=95009907; PubMed=7523108;
MEDIINE=95009907; PubMed=7523108;
MEDIINE=95009907; PubMed=7523108;
Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
"Separation and sequencing of familiar and novel murine proteins using preparative two-dimensional gel electrophoresis.";
Electrophoresis 15:735-745(1994).
-!- MISCELIANEOUS: On the 2D-gel the determined pI of this unknown protein is: 6.0, its MW is: 32 KDa.
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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0
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0
 01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Unknown protein from 2D-page of fibroblasts (P32) (Fragment).
 Eukaryota, Metazoa, Arthropoda, Crustacea, Malacostraca,
Eumalacostraca, Eucarida, Decapoda, Pleocyemata, Caridea,
Palaemonoidea, Palaemonidae, Macrobrachium.
 23.7%; Score 14; DB 1; Length 9; 100.0%; Pred. No. 1.4e+05; cive 0; Mismatches 0; Indels
 0; Indels
 Length 9;
 GO; GO: 0007218; P:neuropeptide signaling pathway; IDA
 9 9 AMIDATION.
9 AA; 1133 MW; 845A0729C44441F5 CRC64;
 9 AA; 1102 MW; 7E73EAB6D05B1AAB CRC64;
 23.7%; Score 14; DB 1; Le
100.0%; Pred. No. 1.4e+05;
tive 0; Mismatches 0;
 AL19 CARMA

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TO AL19 CARMA
TO 30-MAY-2000 (Rel. 39, Last sequence update)
TO 70-MAY-2000 (Rel. 39, Last annotation update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 19.
OS Carcinus maenas (Common shore crab) (Green crab).
 9 AA
 TISSUE=Eyestalk;
MEDLINE=21107394; PubMed=11179812;
 [1] =
SEQUENCE, AND MASS SPECTROMETRY.
 Local Similarity 100.
 Conservative
 Neuropeptide; Amidation.
MOD RES 9 9
 STANDARD;
 (Mouse)
 Local Similarity
es 3; Conserv
 NCBI_TaxID=10090;
 NCBI_TaxID=79674;
 EIO 6
 4 EIQ 6
 9 HN 10
 4
 Mus musculus
 UF02 MOUSE
 SEQUENCE
 SEQUENCE
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 SEQUENCE
 Query Match
 Query Match
 P38640;
 RESULT 11
UP02 MOUS M
AC D700 M
DT 01-0CT
DT 01-0CT
DT 01-0CT
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Job time : 6.5 secs
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 "Temporins, antimicrobial peptides from the European red frog Rana
temporaria.";
Eur. J. Biochem. 242:788-792(1996).
 Rana temporaria (European common frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana,
 01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ranatachykinin C (RTK 0).
Rana catesbelana (Bull frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
 TISSUB-Intestine;
Made 191254337; PubMed=2043143;
Made H., Hino J., Minamino N., Kangawa K., Matsuo H.;
Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;
"Isolation of four novel tachykinins from frog (Rana catesbeiana)
brain and intestine.";
Biochem. Biophys. Res. Commun. 177:588-595(1991).
 ·;
 .
 -!- FUNCTION: Has antibacterial activity against Gram-positive bacteria.
 TISSUE-Skin secretion;
MEDLINE=97175050; PubMed=9022710;
Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
Barra D.;
 Length 10;
 23.7%; Score 14; DB 1; Length 10; 60.0%; Pred. No. 7.7e+03; ive 1; Mismatches 1; Indels
 Score 14; DB 1; Length 10;
Pred. No. 7.7e+03;
1; Mismatches 2; Indels
BY SIMILARITY.
LUMENAL (POTENTIAL).
817D0F59D6D69DCS CRC64;
 -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Skin.
-!- SIMILARITY: Belongs to the brevinin family.
Amphibian defense peptide; Antibiotic; Amidation.
MOD_RES 10 10 AMIDATION.
SEQUENCE 10 AA; 1123 MW; 390549B337272457 CRC64;
 30-MAY-2000 (Rel. 39, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
 10 AA.
 10 AA
 PRT;
 PRT;
 23.7%;
 1180 MW;
 2; Conservative
 Query Match
Best Local Similarity 60.0
Matches 3; Conservative
 STANDARD;
 STANDARD;
 SEQUENCE, AND SYNTHESIS.
 1 AVSEIQLM 8
 SISAMQFI 8
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6
10 AA;
 Query Match
Best Local Similarity
 7 LMHNL 11
 1 LLPNL 5
 NCBI_TaxID=8400;
 TKNC_RANCA
P22690;
 TEMK_RANTE
P56923:
 DOMAIN
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 SEQUENCE
 RESULT 15
TKNC_RANCA
 TEMK_RANTE
 Matches
 RESULT 14
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RC TISSUE=Intestine;

RX MBDLINE=9403216, PubMed=8210506;

RA Kangawa K. Kozawa H., Hino J., Minamino N., Matsuo H.;

RT intestine.";

RT intestine.";

RE GOIL PEPT. (4:81-80 (1933).

- - - FUNCTION: Tachykinins are active peptides which excite neurons, evoke behavioral responses, are potent vasodilators and secretagogues, and contract (directly or indirectly) many smooth muscles.

CC -- SIMILARITY: Belongs to the tachykinin family.

CC -- SIMILARITY: Belongs to the tachykinin family.

DR FIR, C61033, C61033.

DR InterPro; IPR002040; Tachy Neurokinin.

DR PRSOITE; PS00267; TACHYKININ, 1.

KW Tachykinin; Neuropeptide, Mindation.

FT MOD RES

Query Match

Best Local Similarity 100.0%; Pred. No. 7.7e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps

Qy 9 HN 10

Db 1 HN 2

Search completed: September 5, 2004, 09:35:03
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Q9eqv3 mus musculu Q49534 mycoplasma

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MEDINE=91378546; PubMed=1898066; Guan A.L., Retrios A.D., Henderson G.N., Markland F.S.Jr., ""Purification and characterization of a fibrinolytic enzyme from venom of the southern copperhead snake (Agkistrodon contortrix contortrix).";
 Fibrinolytic metalloproteinase (Fragment).
Agkierrodon contortrix.
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Lepidosauria, Squamata, Scleroglossa; Serpentes, Colubroidea;
Viperidae, Crotalinae, Agkistrodon.
 Score 27; DB 13; Length 11;
Pred. No. 1.4e+02;
1; Mismatches 1; Indels
 11 11 11 11 11 1209 MW; 7CA02D1D41E8772B CRC64;
 Last sequence update)
Last annotation update)
 Arch. Biochem. Biophys. 289:197-207(1991).
 Q055403
Q15894
Q44468
Q44401
Q97KU3
Q97KU0
Q
 01-MAY_2000 (TrEMBLrel. 13, Created)
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 45.8%;
nilarity 71.4%;
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 OSPS71 agkistrodon
P82081 limmodynast
P82082 limmodynast
P82085 limmodynast
O92766 canusta mig
O92766 canine dist
O71066 canine dist
 Q28742 oryctolagus
Q15891 homo sapien
Q9gd12 linospadix
Q9gcv6 sclerosperm
 Q85631 avian carci
)28742 oryctolagus
 3 ; Search time 27.5 Seconds (without alignments) 137.681 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Description
 5.1.6
Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 1017041 segs, 315518202 residues
 GenCore version
Copyright (c) 1993 - 2004
 5, 2004, 09:30:03
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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 1; Mismatches
 Cytochrome b (Fragment).
Locusta migratoria (Migratory locust)
Mitochondrion.
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 SEQUENCE, AND MASS SPECTROMETRY.
AND MASS SPECTROMETRY.
 33.9%;
 33.9%;
Similarity 66.7%;
4; Conservative 1
 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2003 (TrEMBLrel. 24,
 4; Conservative
 PRELIMINARY;
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Matches 4; Conserv
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 7 LMHNLG 12
 7 LMHNLG 12
 LLTNLG 11
 SEQUENCE FROM N.A.
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LISNLG 7
 NCBI TaxID=39404;
 NCBI_TaxID=7004;
 DYNASTIN 7
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 P82085
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 SEQUENCE, AND MASS SPECTROMETRY.

TISSUE=TIBIAL GLAND;

Raftery M.J., Bradford A.M., Bowie J.H., Wallace J.C., Tyler M.J.;

Peptides from Australian frogs. The structure of the dynastins from the banjo frogs Limnodynastes interioras, Limnodynastes dumerilli and
 Limmodynastes salmini (Salmin's-striped frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Amphibia, Batrachia, Anura, Neobatrachia, Bufonoidea, Myobatrachidae,
 Limnodynastes salmini (Salmin's-striped frog).
Eukaryota, Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Barrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
Limnodynastinae; Limnodynastes.
 Limnodynastes terraereginae (Northen banjo frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
Limnodynastinae; Limnodynastes.
 Gaps
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 ..
 39.0%; Score 23; DB 13; Length 12; llarity 66.7%; Pred. No. 1e+03; Conservative 2; Mismatches 0; Indels
 33.9%; Score 20; DB 13; Length B; 66.7%; Pred. No. 1e+06;
 1; Indels
 Limnodynastes terraereginae.";
Aust. J. Chem. 46:833-842(1993).
Aust. J. Chem. 46:833-842(1993).
SEQUENCE 12 AA; 1236 MW; 147AA70FDF472724 CRC64;
 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DYNASTIN 4.
 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DYNASTIN 3.
 8 A.A.
 Æ
 1; Mismatches
 PRT;
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 SEQUENCE, AND MASS SPECTROMETRY. TISSUE=SKIN SECRETION;
 Limnodynastinae; Limnodynastes.
NCBI TaxID=39404;
 Conservative
 PRELIMINARY;
 PRELIMINARY;
 Best Local Similarity
Matches 4; Conserv
 Local Similarity
 7 LMHNLG 12
 7 LMHNLG 12
 NCBI TaxID=104894;
 6 LLNNLG 11
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 P82083
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RESULT 3 P82082

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Limnodynastes salmini (Salmin's-striped frog).
Eukaryota; Metazoa; Chordata; Craniata; Verrebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
Limnodynastinae; Limnodynastes.
Gaps
 TISSUE-SKIN SECRETION;
Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;
Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;
"Peptides from Australian frogs. The structure of the dynastins from Limnodynastes salmini and Fletcherin from Limnodynastes fletcheri.";
 Gaps
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 ..
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
Acridoidea; Acrididae; Oedipodinae; Locusta.
 Length 12;
 Score 20; DB 13; Length 8; Pred. No. 1e+06; 1; Mismatches 1; Indels
 1; Indels
 Aust. 7. Chem. 46:1235-1244(1993).
-!- MASS SPECTROMETRY: MW=1114; METHOD=FAB.
SEQUENCE 12 AA; 1114 MW; 3AB5A976CAA72728 CRC64;
 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAY-2000 (TrEMBLrel. 13, Last annotation update)
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 Score 20; DB 13;
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
01-OCT-2002 (Fragment)
0272a sativa (Rice)
0772a sativa (Rice)
0772a sativa (Rice)
0772a sativa (Rice)
 SEQUENCE FROM N.A.
MEDLINE-91/08641; PubMed-2258052;
Kumagai M.H., Shah M., Terashima M., Vrkljan Z., Whitaker J.R.,
Rodriquez R.L.,
"Expression and secretion of rice alpha-amylase by saccharomycers
 MEDLINE=92013147; PubMed=1717588;
MEDLINE=92013147; PubMed=1717588;
Takahashi K., Kishimoto S., Ohori K., Yoshizawa H., Machida A., Ohnuma H., Tsudad F., Munekata B., Miyakawa Y., Mayumi M.;
"Molecular heterogeneity of e antigen polypeptides in sera from cartiers of hepatitis B virus.";
J. Immunol. 147.3156-3160(1991).
PIR: B46453; B46453.
 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
E antigen P20E (Fragment).
Hepatitis B virus.
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
NCH_TAXID=10407;
 30.5%; Score 18; DB 12; Length 10; ilarity 60.0%; Pred. No. 8.9e+03; Conservative 1; Mismatches 1; Indels
 30.5%; Score 18; DB 10; Length 8; 28.6%; Pred. No. 1e+06;
 0; Indels
 0; Indels
 Score 19; DB 12; Length Pred. No. 1e+06;
 10 AA; 1238 MW; 485A6E3AE721E9C7 CRC64;
 8 AA; 948 MW; EBC694444732D6D6 CRC64;
32.2%; 'Score' 100.0%; Pred. No. ...
 10 A.A.
 5; Mismatches
 PRT;
 cerevisiae.";
Gene 94:209-216(1990).
EMBL; M62916; AAA33892.1; -.
Gramene; Q40659; -.
 Ouery Match
Best Local Similarity 28.5
Section 2, Conservative
 Query Match
Best Local Similarity 100.
Matches 3; Conservative
 PRELIMINARY;
 PRELIMINARY;
 5 IQLMHNL 11
 Query Match
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Matches 3; Conserv
 1 MOVLNNM 7
 NCBI_TaxID=4530;
 S IQLMH 9
 8 MHN 10
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 SEQUENCE
 Q40659
Q40659;
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Q9PXC3
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 SEQUENCE FROM N.A.
STRAIN=DOG #5266/89
STRAIN=DOG #5266/80
Liermann H. Harder T., Haas L.;
"Genetic analysis of the central untranslated genome region and the proximal config part of the F gene of wild-type and vaccine distemper
 STRAIN=DOG #10757/96;
STRAIN=DOG #10757/96;
Liermann H., Harder T., Haas L.;
Liermann H., Harder T., Haas L.;
Genetic analysis of the central untranslated genome region and the proximal coding part of the F gene of wild-type and vaccine distemper morbilliviruses.";
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.

Submit AF026234; AAC09164.1; -.
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0
 32.2%; Score 19; DB 12; Length 9; llarity 100.0%; Pred. No. 1e+06; Conservative 0; Mismatches 0; Indels
 Canine distemper virus.
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Morbillivirus.
NCBI_TaxID=11232;
 h 32.2%; Score 19; DB 8; Length 8; Similarity 50.0%; Pred. No. 1e+06; 4; Conservative 2; Mismatches 2; Indels
 Canine distemper virus.
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Morbillivirus.
NCBI_TaxID=11232;
 morbilliviruses.";
Submitted (GEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF026237; AAC09167.1; -.
NON TER 9
 8 8 AA; 1019 MW; F8E33723304B45B6 CRC64;
 01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 Last sequence update)
Last annotation update)
 9 AA; 1011 MW; F281732760533441 CRC64;
 9 AA; 1124 MW; F29D045760440441 CRC64;
 9 AA.
 Created)
 01-NOV-1998 (TrEMBLrel, 08, 01-NOV-1998 (TrEMBLrel, 08, 01-NOV-1998 (TrEMBLrel, 08, Fusion protein (Fragment).
 Fusion protein (Fragment).
 PRELIMINARY;
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 Query Match
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 2 VSEIQLMH 9
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1 MSYIKLKH 8
 Local Similarity
 8 MHN 10
 Mitochondrion.
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 SEQUENCE FROM N.A.
MEDLINE=85033920; PubMed=6092695;
Sutrave P., Jansen H.W., Bister K., Rapp U.R.;
Sutrave P., Jansen H.W., Bister K., Rapp U.R.;

"3'-terminal region of avian carcinoma virus MH2 shares sequence elements with avian sarcoma viruses Y73 and SR-A.";

J. Virol. 52:703-705(1984).

EMBL; K03100; AA442388.1; -.
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0
 30.5%; Score 18; DB 15; Length 12; 100.0%; Pred. No. 1.1e+04; tive 0; Mismatches 0; Indels
 Length 11;
 1; Indels
 Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
 SEQUENCE FROM N.A.
MEDLINE=82260445; PubWed=6286214;
MCKGOUN M., Firtel R.A.
"Actin multigene family of Dictyostelium.";
Cold Spring Harb. Symp. Quant. Biol. 46:495-505(1982).
BMBL, K02956; AAA33150.1; JOINED.
BENBL, K02956; AAA33150.1; JOINED.
SEQUENCE 11 AA; 1205 MW; 728B4C14C6C2CAAB CRC64;
 12 AA; 1466 MW; 72E4B884F30736DB CRC64;
 Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MH2, provital DNA, myc to 3' LTR (Fragment).
Avian carcinoma virus.
 01-NOV-1996 (TrEWBLrel. 01, Created) 01-NOV-1996 (TrEWBLrel. 01, Last sequence update) 01-JUN-2003 (TrEWBLrel. 24, Last annotation update) Alpha-myosin heavy chain (Fragment). Oryctolagus cuniculus (Rabbit).
 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 30.5%; Score 18; DB 5; I 28.6%; Pred. No. 9.9e+03; atrive 4; Mismatches 1;
 12 AA
 11 AA
 PRT;
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 Local Similarity 100.
 Local Similarity 28.6 es 2, Conservative
 PRELIMINARY;
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 4 EIQLMHN 10
 5 DVQALNN 11
 NCBI_TaxID=11958;
 NCBI TaxID=44689;
 HNL 11
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SEQUENCE
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 085631;
 028742;
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 023876;
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 Matches
 RESULT 11
223976
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AC 02387
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DT 01-NO
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COX NOB1
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 RESULT 12
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Characterization of genomic clones specifying rabbit alpha- and beta-
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 TISSUBE-Placenta;
Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
 Chloroplast.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Arecaceae; Arecoideae;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
 "Isolation of chromosome-specific genes by reciprocal probing of arrayed cDNAs and cosmid libraries.";

Hum. Mol. Genet. 0:0-0(1995).

EMBL; L32131; AAA73881.1; -.
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 SEQUENCE FROM N.A.
MEDIINE-84221901; PubMed-6328491;
Friedman D.J., Umeda P.K., Sinha A.M., Hsu H.-J., Jokovcic S.,
Rabinowitz M.;
 Indels
 28.8%; Score 17; DB 4; Length 9; 44.4%; Pred. No. 1e+06;
 Score 17; DB 6; Length 7; Pred. No. 1e+06;
 1; Indels
 Q15891;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DBC-2001 (TrEMBLrel. 19, Last annotation update)
(Clone XP2E8B) (Fragment).
 01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
Ribosomal protein S16 (Fragment).
 9 AA; 1030 MW; E56635A1A33686D1 CRC64;
 1 1 7 AA; 916 MW; 6B1B1AA1E69326B0 CRC64;
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 ventricular myosin heāvy chains.";
Proc. Natl. Acad. Sci. U.S.A. 81:3044-3048(1984).
EMBL; K01698; AAA31415.1; -.
PIR; I46868; 146868.
 9 AA.
 1; Mismatches
 2; Mismatches
 PRT;
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 1 28.8%; Similarity 60.0%; 3; Conservative 3;
 Local Similarity 44.4
nes 4; Conservative
 PRELIMINARY;
 PRELIMINARY;
 Linospadix monostachya.
 4 EIQLMHNLG 12
 (Human)
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EHQMKTSLG
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Best Local Similarity
 SEQUENCE FROM N.A.
 6 OLMHN 10
 1 OKWHD 5
 NCBI_TaxID=9606;
 Homo sapiens
 SEQUENCE
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 1586107 seqs, 282547505 residues
 OM protein - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 1 AVSEIQLMHNLG 12
 US-09-730-174A-5
59
 September
 Minimum DB seq
Maximum DB seq
 Title:
Perfect score:
 Scoring table:
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 Run on:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

length: 0 length: 12

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Abg72607 Parathyro
Abg72608 Parathyro
Aay68767 Amino aci
Aab68219 Human par
Abr44166 Human par
Abs6219 Human par
Abs66219 Human par
Aab66000 Resin bou
Aab01862 Pfff(1-14)
Aay6966 Parathyro
Aay69681 Parathyro
Aay66981 Parathyro
Aab66220 Human par
Aab66220 Human par
Aab6632 Rat parathyro
Aab66932 Rat parathyro
Aab66932 Rat parathyro
Aab66931 Rat parathyro
Aab66931 Rat parathyro
Aab66931 Parathyro Parathyro (Asn10, T Rat parat Parathyro Parathyro Aay96968 Parathyro Description Aab84769 I Aaw45785 I Abp71484 1 Aap82547 Aab96892 F Aab96914 SUMMARIES AAY96968 ABG72607 AAG72608 AAX61644 AAY68767 AAY68767 AAX84166 AAB86225 AAY50600 AAB18622 AAY96966 AAR91645 AAB01863 AAY96981 AAB86220 AAB96932 AAB96914 AAB84769 % Query Match Length DB Score Result 

AAB96892

Compounds of the structure or formula S-(L) n-B, R 1-S-(L) n-R or S-(L) n-R, are new. S is an amino terminal signaling functional domain of parathyroid hormone (PTH); L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4); B is a C-terminal binding portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R 1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor signal sequence; nere used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone reformation, bone resorption and/or bone remodeling, treating diseases and disorders associated with decreased tetherl activity, increasing CAMP

| Abp71485 Parathyro<br>Abp71483 Parathyro<br>Aab96891 Rat parat<br>Ahr71482 parathyro | 1864 PTH<br>78849 PAR<br>97062 PTH                       | 67 Antige<br>21 Human<br>66 PTH(1-  | . 4 6 6 7 4 5 E                  |                       |
|--------------------------------------------------------------------------------------|----------------------------------------------------------|-------------------------------------|----------------------------------|-----------------------|
|                                                                                      | 9 3 AAY7884<br>9 3 AAY7884<br>9 3 AAY9706<br>8 2 AAR9164 | 3 AAB0746<br>4 AAB8622<br>3 AAB0186 | 5 ABG985<br>5 ABG985<br>5 ABG985 | 2 H G G G             |
| വവവവ                                                                                 | 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2                    | 1000<br>1000<br>1000<br>1000        | 44.5.                            |                       |
| 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0                                                | 9 8 8 8<br>9 8 8 8                                       | # W W W 4                           | ) W W 4, 4                       | 1 4 4 4 4<br>1 8 4 10 |

## ALIGNMENTS

New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass. PTH; parathyroid hormone; N-terminal; signaling domain; bone mass; bone reformation; resorption; remodeling; tetherl; osteoporosis. Parathyroid hormone N-terminal signaling domain (residues 1-11). Gardella TJ, Kronenberg HM, Potts JT, Jueppner H; AAY96968 standard; peptide; 11 AA Claim 4; Page 92; 119pp; English. 99WO-US031108, 98US-0114577P. (first entry) (GARD/) GARDELLA T J. (KRON/) KRONENBERG H M. (POTT/) POTTS J T. (JUEP/) JUEPPNER H. WPI; 2000-452384/39. WO200039278-A2. 31-DEC-1998; 30-DEC-1999; Homo sapiens 31-OCT-2000 06-JUL-2000. AAY96968 AAY96968  0;

Gaps

; 0

1; Indels

0; Mismatches

Score 50; DB 6; Length 11; Pred. No. 0.012;

8 x 8 8 8 8 8

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the method; and (3) test kits and analytical procedures used for the determination of bioactive intact PTH utilising (ab). The methods and compositions of the present invention are useful for determining bioactive intact PTH levels in serum, plasma and/or cell culture media. The antigens, antibodies and methods of the present invention, as compared to prior art, have the particular advantages of possessing preater affinity for PTH, and in particular, are designed to have a novel recognition for amino acid residues extending beyond the first N-terminal PTH residue, and further have negligible cross-reactivity with the large non-molecular forms of PTH. PTH levels are an important parameter in patients suffering from hypercallacemia, osteoporosis and primary hyperparathyroidism. The present sequence represents a PTH antigenic peptide representing amino acids 2-12 of human, mouse, rat, porcine,
 84.7%;
90.9%;
 10; Conservative
 2 VSEIQLMHNLG 12
 1 VSEIQXMHNLG 11
 ь
С
 canine and bovine PTH
 WPI; 2003-066685/06.
 (ZAHR/) ZAHRADNIK R
(LAVI/) LAVIGNE J R.
 Best Local Similarity
Matches 10; Conserv
 Sus scrofa.
Canis familiaris.
 Misc-difference 7
 Misc-difference
 US2002110871-A1
 Sequence 11 AA;
 Homo sapiens
 11-FEB-2003
 .5-AUG-2002.
 Rattus sp.
Bos taurus.
 ABG72608;
 Query Match
 Mus sp.
 ABG72608
 RESULT
 $$$$$$$$$$$$$$$$$$$
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 g
 The invention relates to a new antigenic peptide for inducing the formation and isolation of antibodies having an affinity to it, being formed from the N-terminus of parathyroid hormone (FTM). Also included are; (1) a method for producing antibodies useful in the determination of PTM levels in a biological sample comprising: (a) providing at least one first peptide antigen comprising a peptide fragment of PTM; (b) administering the first peptide antigen to a host animal to induce antibody production; (c) monitoring the antibody tirre produced; (d) isolating antisera produced in the host animal; and (e) selecting antisera produced in the host animal; and (e) selecting of binding to a second peptide antigen; (2) an antibody (ab) produced by
 0
 in a mammalian cell having PTH-1 receptors, or screening for a peptide or non-peptide PTH (claimed). The new compound can be administered by inhalation unlike the large native PTH or PTHrP which avoids the need for regular injections to treat osteoporosis
 formation
 New parathyroid hormone (PTH) antigenic peptide inducing the formatior and isolation of antibodies having an affinity to it, useful for determining bioactive PTH levels in serum, plasma and/or cell culture
 Gaps
 Human; parathyroid hormone; antigen; hypercalcaemia; osteoporosis; primary hyperparathyroidism; mouse; rat; bovine; porcine; canine.
 .,
0
 89.8%; Score 53; DB 3; Length 11; 100.0%; Pred. No. 0.0034; Live 0; Mismatches 0; Indels
 Parathyroid hormone antigenic peptide 2-12.
 Location/Qualifiers
 ABG72607 standard; peptide; 11 AA.
 /label= Leu, Phe
 Claim 1; Page 5; 11pp; English.
 05-DEC-2000; 2000US-00730174.
 05-DEC-2000; 2000US-00730174
 Zahradnik RJ, Lavigne JR;
 (first entry)
 11; Conservative
 1 AVSEIQLMHNL 11
 1 AVSEIGLMHNL 11
 ZAHRADNIK R J.
LAVIGNE J R.
 WPI; 2003-066685/06.
 Query Match
Best Local Similarity
Matches 11; Conserv
 Rattus sp.
Bos taurus.
Sus scrofa.
Canis familiaris.
 Misc-difference
 US2002110871-A1
 Sequence 11 AA;
 Homo sapiens.
 15-AUG-2002.
 11-FEB-2003
 ABG72607;
 (ZAHR/)
 (LAVI/)
 Mus sp.
 media.
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New parathyroid hormone (PTH) antigenic peptide inducing the formation and isolation of antibodies having an affinity to it, useful for determining bioactive PTH levels in serum, plasma and/or cell culture
 Human; parathyroid hormone; antigen; hypercalcaemia; osteoporosis; primary hyperparathyroidism; mouse; rat; bovine; porcine; canine.
 Parathyroid hormone antigenic peptide 1-12.
 Location/Qualifiers
Ä
 label= Ser, Ala
 /label= Leu, Phe
 Claim 2; Page 5; 11pp; English
ABG72608 standard; peptide; 12
 05-DEC-2000; 2000US-00730174.
 05-DEC-2000; 2000US-00730174.
 Zahradnik RJ, Lavigne JR;
 (first entry)
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an

injecting

The present sequence is a specific example of claimed immunogenic peptides having a sequence from hPTH(1-37) which includes the N- of terminal alpha-helical region and/or the non-structured region of hormone. Antibodies and their binding fragments generated by inject animal with the peptides are useful as diagnostic reagents for determination of biologically active hPTH(1-37)

Sequence 10 AA;

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The invention relates to a new antigenic peptide for inducing the formation and isolation of antibodies having an affinity to it, being formation and isolation of antibodies having an affinity to it, being are; (1) a method for producing antibodies useful in the determination of first peptide antigen comprising a peptide fragment of PTH; (b) each antibody production; (c) monitoring the antibody titre produced; (d) isolating antisers produced in the host animal; and (e) selecting antisers produced in the host animal; and (e) selecting antisers produced in the host animal; and (e) selecting antisers produced in the host thing to a second peptide antigen; (2) an antibody (ab) produced by the method; and (3) test kits and analytical procedures used for the offermination of bioactive intact PTH uilising (ab). The methods and compositions of the present invention are useful for determining bloactive intact PTH uilising (ab). The methods and composition of produces and methods of the present invention, as composition for amino acid residues extending beyond the first Niterminal procedure affinity for PTH, and in particular, are designed to have a novel of amino and further have the particular, are designed to have a nonelled for amino acid residues extending beyond the first Niterminal promines suffering from hypercalcamia, osteoporosis and primary perpented representing amino acids l-12 of human, mouse, rat, porcine, but the present sequence represents a primary procedure pTH.

Sequence 12 AA;

Score 50; DB 6; Length 12; Pred. No. 0.014; 1; Indels 0; Mismatches 84.7%; 90.9%; Query Match
Best Local Similarity 90.9
Matches 10; Conservative 2 VSEIQLMHNLG 12 2 VSEIQXMHNLG 12 à dd

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Gaps

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AAR91644 standard; peptide; 10 AA. AAR91644; RESULT 4 AAR91644 

Human parathyroid hormone antigenic peptide hPTH 1-10. 06-NOV-1996

Human parathyroid hormone, hPTH; antigen; alpha-helix; immunogen; diagnosis; active hPTH 1-37.

Synthetic.

04-APR-1996.

94DE-04434551 28-SEP-1994;

94DE-04434551 28-SEP-1994;

(FORS/) FORSSMANN W.

Maegerlein M; Hock D, Forssmann W, Adermann K,

New antigenic peptide(s) from human parathyroid hormone - and antibodies generated using them, able to distinguish between active and inactive

WPI; 1996-180391/19.

Claim 2; Page 4; 5pp; German

forms of the hormone

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 o;
 The present sequence represents a parathyroid hormone (pTH) fragment, comprising amino acids 1-10. Parathyroid hormone fragments of the invention have lipolysis stimulating activity (especially when topically administered). The lipolytic activity of the peptides is enhanced when they are chemically modified to increase their lipophilicity. The peptides are used in cosmetic or dermatological compositions for skin care. They are especially used for slimming treatment of excessive weight in the thighs and hips, in the treatment of cellulite and for skin
 New parathyroid hormone fragment peptides, used as lipolysis stimulants in topically applied cosmetic compositions for slimming treatment of excessive weight in hips and thighs.
 Gaps
 Parathyroid hormone; lipolysis; cosmetic; dermatological; skin care; slimming treatment; cellulite; skin firming.
 ..
0
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0
Score 46; DB 2; Length 10;
Pred. No. 0.061;
1; Mismatches 0; Indels
 78.0%; Score 46; DB 3; Length 10; 90.0%; Pred. No. 0.061; 0; Indels:ive 1; Mismatches 0; Indels
 Amino acids 1-10 of a parathyroid hormone (pTH).
 AAY68767 standard; peptide; 10
 Claim 1; Page 8; 18pp; French
/ Match
Local Similarity 90.0%;
les 9; Conservative 1
 99WO-FR001687
 05-MAY-2000 (first entry)
 9; Conservative
 10
 10
 10
 1 AVSEIQLMHN
 WPI; 2000-171243/15
 1 AVSEIQLMHN
 Query Match
Best Local Similarity
 WO200004047-A1.
 (SEDE-) SEDERMA
 Sequence 10 AA;
 17-JUL-1998;
 Unidentified.
 07-JUL-1999;
 27-JAN-2000
 Lintner K;
 AAY68767;
 Query Match
 Best Loc
Matches
 Best Loc
Matches
 RESULT 5
 AAY68767
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AAB86219

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Novel fusion peptide comprising self cell-penetrating Tat peptide bound to human parachyroid hormone-derived peptide, useful as component of skin slimming cosmetic composition.
 The invention relates to a fusion peptide (Tat-hPTHDP), where self cellpenetrating Tat peptide is bound to human parathyroid hormone-derived peptide (hPTHDP). The fusion peptide is useful as a component of skin slimming cosmetic composition. The fusion peptide does not cause irritation, easily and safely penetrates into integument and endotholium, does not cause skin disease and has superior lipolysis effects, and is durable. The present sequence represents a human parathyroid hormone (hPTH) fragment that can be used to construct the fusion peptide
 Fusion peptide; tat; hPTHDP; parathyroid hormone; skin; cosmetic; lipolysis; human; hPTH.
 Parathyroid hormone; hPTH; immunogenic peptide; human; epitope; diagnosis; calcium-metabolism disorder; osteopathy; antagonist; hypo-parathyroidism; hyper-parathyroidism.
 Human parathyroid hormone (hPTH) fragment (residues 1-10)
 78.0%; Score 46; DB 6; Length 10; 90.0%; Pred. No. 0.061; ive 1; Mismatches 0; Indels
 Human parathyroid hormone immunogenic peptide SEQ ID 7.
 Cho W, Kang S,
 (GLDS) LG HOUSEHOLD & HEALTH CARE LTD.
 AAB86225 standard; peptide; 9 AA.
 Claim 5; Page 6; 32pp; English.
 06-MAY-2002; 2002WO-KR000835.
 27-SEP-2001; 2001KR-00060245.
15-MAR-2002; 2002KR-00014062.
 (first entry)
04-AUG-2003 (first entry)
 Kang N, Park S,
 Query Match
Best Local Similarity 90.0
Matches 9; Conservative
 10
 SVSEIQLMHN 10
 WPI; 2003-468288/44.
 1 AVSEIQLMHN
 WO2003035697-A1.
 Sequence 10 AA;
 DE19961350-A1.
 Homo sapiens.
 03-SEP-2001
 01-MAY-2003.
 AAB86225;
 Song Y,
Chang M;
 Homo
 RESULT 8
 AAB8622
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 g
 This invention describes a novel method for determining (M1) the content of active parathyroid hormone (A) by treating a sample with (i) antibody (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A), and including the N-terminal residue and (ii) antibody (Ab2) that recognizes an epitope within the receptor-binding site of (Ab2) that react with both antibodies is determined and used to calculate the content of physiologically active (A). The method is used for diagnosis of calcium-metabolism disorders, osteopathy, or hypo- or hyper-parathyroidism. The method (unlike known assays) recognizes that (i) some fragments of (A) shorter than the complete (84 aa) peptide are cotive and (ii) that apparently intact peptide may be biologically are antagonistic (these have the receptor-binding site but lack the N-terminus). It thus provides a true measure of the content of physiologically active (A); contrast methods that measure intact peptide sequence represents a peptide fragment used to illustrate the method of the invention
 ö
 Determining the content of physiologically active parathyroid hormone, useful in diagnosis of calcium-metabolism disorders, using two antibodies reactive with different epitopes.
 Gaps
 Parathyroid hormone; hPTH; immunogenic peptide; human; epitope; diagnosis; calcium-metabolism disorder; osteopathy; antagonist; hypo-parathyroidism; hyper-parathyroidism.
 ö
 78.0%; Score 46; DB 4; Length 10; 90.0%; Pred. No. 0.061; O: Indels ive 1; Mismatches 0; Indels
 Human parathyroid hormone immunogenic peptide SEQ ID 1.
 AAB86219 standard; peptide; 10 AA
 Disclosure; Page 3; 10pp; German.
 99DE-01061350.
 99DE-01061350.
 (IMMU-) IMMUNDIAGNOSTIK AG.
 (first entry)
 9; Conservative
 1 AVSEIQLMHN 10
 SVSEIOLMHN 10
 WPI; 2001-376318/40.
 Best Local Similarity
 Sequence 10 AA;
 Armbruster FP;
 DE19961350-A1
 Homo sapiens.
 17-DEC-1999;
 17-DEC-1999;
 03-SEP-2001
 21-JUN-2001.
 AAB86219;
 Query Match
```

Min H;

Lim J,

Lee Y,

ö

Gaps

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99DE-01061350.

17-DEC-1999;

21-JUN-2001

ABR44166 standard; peptide; 10 AA.

RESULT 7 ABR44166

Matches

ઠે 셤 ABR44166

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This invention describes a novel method for the preparation of peptides (II) that contain both cyclic and linear peptide fragments comprises sequential reaction of a real-bound linear fragment with the cyclic sequential reaction of a real-bound linear fragment with the cyclic fragments in N-protected form and optionally other linear fragments. The creation have osteopathic and hypotensive activity. (II) bind to hPTH receptors and act as agonises or antagonises of hPTH. The method is particularly used to prepare cyclic peptide analogs of parathyroid hormone (PTH) or PTH-related peptides which are useful for treathyroid hormone (PTH) or PTH-related peptides which are useful for receptors (with or without activation of adenylyl cyclase activity), e.g. hyper- or hypo-calcemia, osteoporosis, osteopenia, hyper- or hypo-for parathyroidism, Cushing's syndrome, renal fallure and hypertension, also for promoting repair of bone fractures. Separate synthesis of the cyclic fragment allows convergent synthesis of resin-bound (III), with better cycled and higher throughput. The difficulties associated with preparation of the bridged fragment are confined to a small peptide which is preparation of the peptide fragments described in the method of the
 Convergent synthesis of peptides for treating e.g. bone disorders.
 Parathyroid hormone peptide, PTH, PTH-related peptide, PTHrP, calcium homeostasis, PTH-1 receptor, PTH-2, vitamin D synthesis, bone synthesis, agonist, osteoporosis, non-parenteral delivery.
 Score 43.5; DB 2; Length 11; Pred. No. 0.2;
 PTH(1-14)/PTHrP(1-14)-derived peptide, SEQ ID NO:6.
 Mismatches
 (RHON) RHONE-POULENC RORER PHARM INC.
 Disclosure, Page 75; 85pp; English.
 /note= "Asn(Trt)"
 AAB01862 standard; peptide; 9 AA
 ;
 99WO-US008435
 98US-0081897P
 99WO-US024481.
 Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
 11-SEP-2000 (first entry)
 Sledeski AW, Mencel JJ;
 1 AVSEIQLMHNLG 12
 11
 1 AVSEIQL-HNLG
 WPI; 1999-633822/54
 Sequence 11 AA;
 WO200023594-A1.
 15-APR-1998;
 15-APR-1999;
 WO9952933-A1
 20-OCT-1999;
 sapiens
 27-APR-2000
 invention
 AAB01862;
 Ношо
 RESULT 10
 AAB01962

1D AAB0

XX AX

XX AAB0

XX XX

XX XX

XX XX

XX XX

XX Para

XX Color

YX YX

YX Y
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 g
 This invention describes a novel method for determining (M1) the content of active parathyroid hormone (A) by treating a sample with (i) antibody and including the N-terminal residue and (ii) antibody (AD2) that recognizes the epitope formed by amino acids (aa) 1-3 of (A), and including the N-terminal residue and (ii) antibody (AD2) that recognizes an epitope within the receptor-binding site of (A). The number of molecules that react with both antibodies is determined and used to calculate the content of physiologically active (A). The method is used for diagnosis of calcium-metabolism disorders, osteopathy, or hypo- or hyper-parathyroidism. The method (unlike known assays) recognizes that (i) some fragments of (A) shorter than the complete (A9 as) peptide are active and (ii) that apparantly intact peptide may be biologically inactive, and also takes into account the fact that some fragments of (A) are antagonistic (these have the receptor-binding site but lack the N-terminus). It thus provides a true measure of the content of physiologically active (A); contrast methods that measure intact peptide and its 1-37 fragment which may produce falsely high values. This sequence represents a peptide fragment used to illustrate the method of the invention
 ô
 Determining the content of physiologically active parathyroid hormone, useful in diagnosis of calcium-metabolism disorders, using two antibodies
 Cyclic peptide, resin bound, parathyroid hormone, osteopathic, disease, hypotensive, PTH receptor, treatment, hyper-ad-cemia, hypo-calcemia, osteoporosis, osteopenia, hyper-parathyroidism, hypo-parathyroidism, Cushing's syndrome, renal failure, hypertension, bone fracture repair.
 Gaps
 ..
 76.3%; Score 45; DB 4; Length 9; 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0; Indels
 Location/Qualifiers
 /note= "Glu(OtBu)"
 AAY50600 standard; peptide; 11 AA.
 note= "FMOC-Ala"
 note= "Gln(Trt)"
 reactive with different epitopes.
 Disclosure; Page 3; 10pp; German.
 'note= "His(Trt)"
 Resin bound cyclic peptide 33.
 99DE-01061350
 (IMMU-) IMMUNDIAGNOSTIK AG
 09-FEB-2000 (first entry)
 Query Match 76.3
Best Local Similarity 100.
Matches 9; Conservative
 'note=
 2 VSEIQLMHN 10
 σ
 WPI; 2001-376318/40.
 1 VSEIQLMHN
 Misc-difference 10
 Key
Misc-difference
 Misc-difference
 Misc-difference
 Misc-difference
 Misc-difference
 Armbruster FP;
 Sequence 9 AA;
17-DEC-1999;
 AAY50600;
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RESULT 9 AAY50600

HELLELE ELECTION OF THE STATE O

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Gaps

7

0; Indels

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PTH; parathyroid hormone; N-terminal; signaling domain; bone mass;
 Parathyroid hormone N-terminal signaling domain (residues 1-9).
 Disclosure, Page 26; 73pp; English
 AAY96966 standard; peptide; 9 AA,
 PTH-1/PTH-2 receptor agonists
 Gardella TJ, Kronenberg HM,
 (first entry)
 Query Match 72.9
Best Local Similarity 100.
Matches 9; Conservative
 (GARD/) GARDELLA T J.
(KRON/) KRONENBERG H M.
 1 AVSEIQLMH 9
 WPI; 2000-339693/29
 AVSEIQLMH
 POTTS J T.
JUEPPNER H.
 Sequence 9 AA;
 22-OCT-1998;
 31-OCT-2000
 AAY96966;
 (KRON/)
(POTT/)
(JUEP/)
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Compounds of the structure or formula S-(L) n-B, R-1-S-(L) n-R or S-(L) n-R, are new. S is an amino terminal signaling functional domain of parathyroid hormone (PTH); L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4); B is a C-terminal binding portion of PTH(1-34) or a PTH-related protein (PTH-P) (1-34); R 1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor sequence. The new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone reformation, bone resorption and/or bone remodeling, treating diseases and disorders associated with decreased tetherl activity, increasing cAMP in ammmalian cell having PTH-1 receptors, or screening for a peptide or non-peptide PTH (claimed). The new compound can be administered by inhalation unlike the large native PTH or PTH-P which avoids the need for regular injections to treat osteoporosis
 New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass.
 Human parathyroid hormone; hPTH; antigen; alpha-helix; immunogen; diagnosis; active hPTH 1-37.
bone reformation; resorption; remodeling; tetherl; osteoporosis.
 Human parathyroid hormone antigenic peptide hPTH 1-9.
 72.9%; Score 43; DB 3; Le 100.0%; Pred. No. 1.4e+06;
 100.0%; Preq. w. 100.0%; rive 0; Mismatches
 Sardella TJ, Kronenberg HM, Potts JT,
 AAR91645 standard; peptide; 9 AA.
 Claim 4; Page 92; 119pp; English
 98US-0114577P.
 99WO-US031108.
 (first entry)
 Query Match
Best Local Similarity 100..
 GARDELLA T J.
KRONENBERG H M.
 WPI; 2000-452384/39
 1 AVSEIQLMH
 1 AVSEIQLMH
 JUEPPNER H.
 WO200039278-A2.
 Sequence 9 AA;
 Homo sapiens.
 30-DEC-1999;
 31-DEC-1998;
 96-T-AON-90
 06-JUL-2000
 AAR91645;
 (POTT/)
 GARD/)
 KRON/)
 RESULT 12
AAR91645
 ò
 The invention relates to a novel parathyroid hormone (PTH) peptide (AAB01859) and parathyroid hormone-related peptide (PTHPP; AAB01860), and biologically active derivatives thereof (AAB01857-B01858, AAB01860), and biologically active derivatives thereof (AAB01857-B01858, AAB01860). The peptides of the invention are at least 85% identical to the generic peptide of the formula: XI-Val-Ser-Glu-X2-Gln-Leu-X3-His-X4-X5-CG Ty-Lys-X6 (AB01887), where: XI is Ser or Als; X2 is His or Ser; Met, Leu or NIe; X4 is Asn or ASP; X5 is Leu or Lys; X6 is His or Ser; provided that the peptide is not PTHPP(I-14). The peptides of the invention also encompass fragments of peptides of the invention consisting of amino acids 1-9, 1-10, 1-11, 1-12 and 1-13, and N- and C-terminal derivatives. PTH is a major regulator of calcium homeostasis, and is necessary for the normal function of the gastrointestinal, selection systems. It binds to both PTH-1 receptors on osteoblasts and renal tubular cells, and to the recently identified PTH-2 receptor: PTH has a potent anabolic and to the recently recently receptors on osteoblasts and renal tubular cells.
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 phosphate clearance and vitamin D synthesis in the kidney. A homologous calls of protein hormones, the PTH-related proteins (PTH-P) mimic some of the renal and skeletal actions of PTH, and also bind to the PTH-1 receptor. They do not bind to the PTH-2 receptor. They do not bind to the PTH-1 receptor. The peptides of the invention are either agonists of PTH-1 and PTH-2 receptors (AABO1865, AABO1861-B01866) or are PTH-1/PTH-2 receptor antagonists (AABO1867-B01866). PTH-1/PTH-2 receptor adonists (AABO1867-Gonditions characterised by a decrease in bone mass, such as
 osteoporosis. PTH-1/PTH-2 receptor antegonists are useful for treating medical disorders that arise from excessive or altered action of the PTH-1/PTH-2 receptor. Detectably labelled peptides of the invention are also useful in the determination of rates of bone formation, bone resorption and/or bone remodelling in a patient. The peptides of the invention are minimised, versions of PTH or PTHPP which are inexpensive to prepare by conventional synthetic chemistry, and can be delivered to a patient via non-parenteral routes. Sequences AABO1858 and AABO1861-B01866 represent
 Parathyroid hormone (PTH) peptides, PTH related peptides and the nucleic acids that encode them, useful for treating osteoporosis.
 Gaps
 .,
 72.9%; Score 43; DB 3; Length 9; 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0; Indels
 Jueppner H;
 Potts JT,
 98US-0105530P
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Jueppner H;

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Gaps

. 0

Indels Length 9;

94DE-04434551.

28-SEP-1994;

DE4434551-A1

04-APR-1996.

```
CC (AAB01859) and parathyroid hormone-related peptide (PTHTP, AAB01860), and biologically active derivatives thereof (AAB01857-B01858, AAB01861-CC B01869). The peptides of the invantion are at least 85% identical to the generic peptide of the formula: X1 val -Ser-Glu-X2-Glu-Leu-X3-His-X4-X5-Gly-Lys-X6 (AAB01857) where: X1 is Ser or Ala; X2 is Ile or Lys; X3 is Net, Leu or Nle; X4 is Aan or Asp; X5 is Leu or Lys; X6 is His or Ser; provided that the peptide is not PTHTP[1-14]. The peptides of the invention also encompass fragments of peptides of the destroint strain of amino acids 1-9, 1-10, 1-11, 1-12 and 1-13, and N- and C-terminal derivatives. PTH is a major regulator of calcium homeostasis, and is necessary for the normal function of the gastrointestinal, seleted, neurological system, neuromuscular and cardiovascular systems. It binds to both PTH-1 receptors on osteoblasts and renal tubular cells, and to the recently identified PTH-2 receptor. PTH has a potent anabolic effect on the skeleton, and mediates calcium reabsorption, enhances phosphate clearance and vitamin D synthesis in the kidney. A homologous calls of protein knormones, the PTH-2 receptor The peptides of the receptor. They do not bind to the PTH-2 receptor antagonists (AAB01856, AAB01865) or are either agonists of PTH-2 receptor antagonists are useful for treatment of conditions characterised by a decrease in bone mass, such as conditions characterised by a decrease in bone mass, such as conditions characterised by a decrease in bone mass, such as conditions characterised by a decrease in bone mass, such as conditions characterised by a decrease in bone mass, such as conditions characterised by a decrease in bone mass, such as compared by the preceptor antagonists are useful for treatment of ceptors. PTH-1/PTH-2 receptor artagonists of the invention are also useful in the determination
 Gaps
 PTH; parathyroid hormone; N-terminal; signaling domain; bone mass;
bone reformation; resorption; remodeling; tetherl; osteoporosis.
 .
0
 Score 40; DB 3; Length 9;
Pred. No. 1.4e+06;
1; Mismatches 0; Indels
 Parathyroid hormone N-terminal signaling domain.
 AAY96981 standard; peptide; 9 AA.
 non-parenteral routes. Sequend
PTH-1/PTH-2 receptor agonists
 98US-0114577P.
 67.8%;
 88.98;
 (first entry)
 Conservative
 (GARD/) GARDELLA T J. (KRON/) KRONENBERG H M.
 σ
 POTIS J I.
JUEPPNER H.
 Best Local Similarity
Matches 8; Conserv
 1 AVSEIQLMH
 WO200039278-A2.
 Sequence 9 AA;
 Homo sapiens.
 30-DEC-1999;
 31-DEC-1998;
 31-OCT-2000
 06-JUL-2000.
 AAY96981;
 Query Match
 (KRON/)
(POTT/)
(JUEP/)
 RESULT 14
 AAY96981
 88999999999999999999999999999999
 Dp
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 an
 New antigenic peptide(s) from human parathyroid hormone - and antibodies generated using them, able to distinguish between active and inactive forms of the hormone.
 related peptides and the nucleic
 The present sequence is a specific example of claimed immunogenic peptides having a sequence from hPTH(1-37) which includes the N- or C-terminal alpha-helical region and/or the non-structured region of the hormone. Antibodies and their binding fragments generated by injecting animal with the peptides are useful as diagnostic reagents for determination of biologically active hPTH(1-37)
 Gaps
 Parathyroid hormone peptide, PTH, PTH-related peptide, PTHrP, calcium homeostasis, PTH-1 receptor; PTH-2; vitamin D synthesis, bone synthesis; agonist; osteoporosis; non-parenteral delivery.
 ..
 Score 40; DB 2; Length 9;
 Parathyroid hormone (PTH) peptides, PTH related peptides acids that encode them, useful for treating osteoporosis
 Ξ
 PTH(1-14)/PTHrP(1-14)-derived peptide, SEQ ID NO:7.
 Maegerlein M;
 Jueppner
 1; Mismatches
 Potts JT,
 Ď,
 Disclosure, Page 26, 73pp, English.
 Hock
 AAB01863 standard; peptide; 9 AA.
 94DE-04434551.
 Claim 2; Page 4; 5pp; German.
 67.8%;
 Gardella TJ, Kronenberg HM,
 98US-0105530P
 99WO-US024481
 Forsamann W,
 11-SEP-2000 (first entry)
 Query Match
Best Local Similarity 88.9
Matches 8; Conservative
 (GARD/) GARDELLA T J.
(KRON/) KRONENBERG H M.
(POTT/) POTTS J T.
 1 AVSEIQLMH 9
 σ
 (FORS/) FORSSMANN W.
 WPI; 1996-180391/19.
 SVSEIOLMH
 JUEPPNER H.
 WPI; 2000-339693/29
 WO200023594-A1
 Sequence 9 AA;
 28-SEP-1994;
 sapiens.
 20-0CT-1999;
 Adermann K,
 22-OCT-1998;
 27-APR-2000.
 Synthetic
 AAB01863;
 (KRON/)
(POTT/)
(JUEP/)
 RESULT 13
 Ношо
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Jueppner H;

Potts JT,

Kronenberg HM,

Sardella TJ,

The invention relates to a novel parathyroid hormone (PTH) peptide

```
WPI; 2000-452384/39.
```

New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass.

Claim 11; Page 93; 119pp; English

Compounds of the structure or formula S-(L) n-B, R 1-S-(L) n-R or S-(L) n-R or S-(L

Sequence 9 AA;

ô Gaps . 0 0; Indels Length 9; Score 40; DB 3; I Pred. No. 1.4e+06; 1; Mismatches Query Match 67.8%; Best Local Similarity 88.9%; Matches 8; Conservative

1 AVSEIQLMH 9

1 SVSEIQLMH 9

g ò

AAB86220 standard; peptide; 9 AA. 

AAB86220;

03-SEP-2001 (first entry)

Human parathyroid hormone immunogenic peptide SEQ ID 2.

Parathyroid hormone; hPTH; immunogenic peptide; human; epitope; diagnosis; calcium-metabolism disorder; osteopathy; antagonist; hypo-parathyroidism; hyper-parathyroidism.

Homo sapiens

DE19961350-A1

21-JUN-2001.

99DE-01061350 17-DEC-1999;

99DE-01061350. 17-DEC-1999;

(IMMU-) IMMUNDIAGNOSTIK AG.

Armbruster FP;

WPI; 2001-376318/40.

Determining the content of physiologically active parathyroid hormone, useful in diagnosis of calcium-metabolism disorders, using two antibodies reactive with different epitopes.

Disclosure, Page 3; 10pp; German.

This invention describes a novel method for determining (M1) the content of active parathyroid hormone (A) by treating a sample with (i) antibody

and including the N-terminal residue and (ii) antibody (Ab2) that
conditions an epitope within the receptor-binding site of (A). The number
confidence is that react with both antibodies is determined and used to
confidence the content of physiologically active (A). The method is used
for diagnosis of calcium-metabolism disorders, osteopathy, or hypo-or
hyper-parathyroidism. The method (unlike known assays) recognizes that
chyper-parathyroidism. The method (unlike known assays) recognizes that
chyper-parathyroidism.
The method (unlike known assays) recognizes that
chyper-parathyroidism at that the complete (84 aa) peptide are
active and (ii) that apparently intact peptide may be biologically
inactive, and also takes into account the fact that some fragments of (A)
are antagonistic (these have the receptor-binding site but lack the Ntermins). It thus provides a true measure of the content of
thysiologically active (A); contrast methods that measure intact peptide
sequence represents a peptide fragment used to illustrate the method of
the invention ö Gaps ö Score 40; DB 4; Length 9; Pred. No. 1.46+06; 1; Mismatches 0; Indels 1; Mismatches 5, 2004, 09:34:30 67.8%; Search completed: September Job time : 36.5 secs Φ 1 AVSEIQLMH 1 SVSEIQLMH Sequence 9 AA; g ò

```
September 5, 2004, 09:37:09; Search time 32.5 Seconds (without alignments) 116.332 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 OM protein - protein search, using sw model
 Run on:
```

BLOSUM62 Gapop 10.0 , Gapext 0.5 US-09-730-174A-5 59 1\AVSEIQLMHNLG 12 Scoring table: Perfect score: Sequence:

Total number of hits satisfying chosen parameters: 1298764 segs, 315065143 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

| Cgn2\_6/ptodata/2/pubpaa/USO7 PUBCOWB.pep:\*
| Cgn2\_6/ptodata/2/pubpaa/USO7 FUB PUB.pep:\*
| Cgn2\_6/ptodata/2/pubpaa/USO6 FUB PUB.pep:\*
| Cgn2\_6/ptodata/2/pubpaa/USO6 FUB PUB.pep:\*
| Cgn2\_6/ptodata/2/pubpaa/USO6 FUB PUB.pep:\*
| Cgn2\_6/ptodata/2/pubpaa/USO8 FUB COMB.pep:\*
| Cgn2\_6/ptodata/2/pubpaa/USO8 FUB PUB.pep:\*
Published Applications\_AA:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

| Description                    | Segmence 5. Appli | 'n               | -                | Sequence 6. Appli | 4                | ,                | , H             | ,               | 9               | œ               | 7               | ` ~             | œ               | 'n              | 10,              | : |
|--------------------------------|-------------------|------------------|------------------|-------------------|------------------|------------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|------------------|---|
| QI                             | US-09-730-174A-5  | US-09-730-174A-3 | US-09-730-174A-1 | US-09-730-174A-6  | US-09-730-174A-4 | US-09-730-174A-2 | US-10-168-185-1 | US-10-168-185-7 | US-10-192-673-6 | US-10-168-185-8 | US-10-192-673-7 | US-10-168-185-2 | US-10-192-673-8 | US-10-168-185-3 | US-10-192-673-10 |   |
| DB                             | 0                 | σi               | σı               | σ'n               | σ                | σ                | 14              | 14              | 14              | 14              | 14              | 14              | 14              | 14              | 14               |   |
| .*<br>Query<br>Match Léngth DB | 12                | 12               | 11               | 12                | 12               | 11               | 10              | 9               | 9               | œ               | o,              | σı              | o               | œ               | σ                |   |
| %<br>Query<br>Match            | 100.0             | 94.9             | 93.2             | 93.2              | 88.1             | 86.4             | 78.0            | 76.3            | 72.9            | 69.5            | 67.8            | 67.8            | 55.9            | 54.2            | 50.8             |   |
| Score                          | 59                | 56               | 52               | 55                | 52               | 51               | 46              | 45              | 43              | 41              | . 40            | 40              | 33              | 32              | 30               |   |
| Result<br>No.                  | H                 | 7                | м                | 4                 | S                | 9                | 7               | 60              | σ               | 10              | 11              | 12              | 13              | 14              | 15               |   |

| Sequence 16, Appl<br>Sequence 4, Appli<br>Sequence 75, Appl<br>Sequence 75, Appl<br>Sequence 77, Appl                           | equence 93<br>equence 61<br>quence 6,<br>equence 74 | 73                                                                                                                                                        | 444004                                                                                                     | Sequence 12, Appl<br>Sequence 12, Appl<br>Sequence 332, Appl<br>Sequence 4, Appli<br>Sequence 11, Appl<br>Sequence 288, Appl<br>Sequence 50, Appl<br>Sequence 249, Appl |
|---------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 12 14 US-10-319-130-16<br>7 14 US-10-168-185-4<br>10 16 US-10-433-234A-75<br>10 16 US-10-432-234A-76<br>10 16 US-10-432-234A-76 | 94 944                                              | 11 12 US-09-874-350A-151<br>10 9 US-09-826-290-27<br>10 16 US-10-264-309-36<br>11 12 US-10-609-217-41<br>11 12 US-10-632-388-41<br>11 12 US-10-651-723-41 | 12 US-10-645-761-4<br>16 US-10-666-696-4<br>14 US-10-286-457-4<br>14 US-10-168-185-5<br>14 US-10-286-457-4 |                                                                                                                                                                         |
| ийиии                                                                                                                           | 72222<br>7222<br>7222<br>7444                       |                                                                                                                                                           | 0 0 0 0 0 0 0 0<br>4 4 4 4 6 6 6 6                                                                         | 3.88<br>4.43<br>4.43<br>5.23<br>6.64<br>6.64<br>6.64<br>6.64<br>6.64<br>6.64<br>6.64<br>6.6                                                                             |

## ALIGNMENTS

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Sequence 5, Application US/09730174A
Patent No. US20020110871A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL TITLE OF INVENTION:
TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having (FILE REPERENCE: IMUNE-001A
CURRENT APPLICATION NUMBER: US/09/730,174A
CURRENT FILING DATE: 2000-12-05
NUMBER OF SEQ ID NOS: 12
LENGTH: 12
 TYPE: PRT:
CRGANISM: Artificial Sequence
FATURE:
CHEANISM: Artificial Sequence
FATURE:
CHEANISM: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-5
 ö
 Gaps
 Query Match 100.0%; Score 59; DB 9; Length 12; Best Local Similarity 100.0%; Pred. No. 0.00072; Matches 12; Conservative 0; Mismatches 0; Indels
US-09-730-174A-5
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1 AVSEIQLMHNLG 12 d à

RESULT 2
US-09-730-174A-3
US-09-730-174A-3
'Sequence 3, Application US/09730174A
'Sequence 3, Application US/09730174A
'Sequence 3, Application US/097108.
'GENERAL INFORMATION:
'APPLICANT: Zahradnik, R.J.
'TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid HC
'FILE REFERENCE: INUNE-001A

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US-09-730-174A-2
US-09-730-174A-2
US-09-730-174A-2
Sequence 2, Application US/09730174A
Patent No. US20020110871A1
GENERAL INFORMATION:
APPLICANY: Zahradnik, R.J.
TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Ho
FILE REFERENCE: IMUNE DATE: US/09/730,174A
CURRENT APPLICATION NUMBER: US/09/730,174A
CURRENT APPLICATION SELECTION NUMBER: US/09/730,174A
NUMBER: OF SEQ ID NOS: 12
 Sequence 4, Application US/09730174A

Patent No. US20020110871A1

GENERAL INFORMATION:

APPLICANT: Zahradnik, R.J.

APPLICANT: Zahradnik, R.J.

TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Ho FILE REFERENCE: IMUNE-001A

CURRENT APPLICATION NUMBER: US/09/730,174A

CURRENT FILING DATE: 2000-12-05

NUMBER OF SEQ ID NOS: 12

SEQ ID NO 4
 ; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies US-09-730-174A-2
 ; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-4
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 Gaps
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 ..
 86.4%; Score 51; DB 9; Length 11; 90.9%; Pred. No. 0.018;
 Indels
 Length 12;
 1; Indels
 APPLICANT: Armbruster, Franz Paul
APPLICANT: Missbichler, Albert
APPLICANN: Schmidt-Gayk, Heinrich
APPLICANN: Roth, Heinz-Jurgen
TITLE OF INVENTION: Method for Determining Parathormone
 Score 52; DB 9;
Pred. No. 0.013;
 0; Mismatches
 1; Mismatches
 ; Sequence 1, Application US/10168185; Publication No. US20030175802A1; GENERAL INFORMATION:
 TYPE: PRT
ORGANISM: Artificial Sequence
 TYPE: PRT
ORGANISM: Artificial Sequence
 Match 88.1%;
Local Similarity 83.3%;
nes 10; Conservative
 Query Match
Best Local Similarity 90.9
Matches 10; Conservative
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 1 SVSEIQFMHNLG 12
 1 AVSEIOFMHNLG 12
 2 VSEIQLMHNLG 12
 1 VSEIOFMHNLG 11
1 AVSEIQLMHNLG
 RESULT 5
US-09-730-174A-4
 RESULT 7
US-10-168-185-1
 SEQ ID, NO 2
 Query Match
 Matches
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 US-09-730-174A-6
US-09-730-174A-6
Sequence 6, Application US/09730174A
Sequence 6, Application US/09730174A
Sequence 6, Application US/09730174A
Sequence 6, Application US-09730174A
Sequence 7. Partial Color Co
 Sequence 1, Application US/09730174A

Patent No. US20020110871A1

GENERAL INFORMATION:

APPLICANT: Zahradnik, R.J.

TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a

TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid HG

FILE REPRENEUE: IMMNE-001A

CURRENT FILING DATE: 2000-12-05

NUMBER OF SEQ ID NOS: 12
 ; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies US-09-730-174A-6
 , OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies US-09-730-174A-1
 OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
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 Query Match

93.2%; Score 55; DB 9; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.0037;
Matches 11; Conservative 0; Mismatches 1; Indels
 Length 11;
 Score 56; DB 9; Length 12;
Pred. No. 0.0025;
 0; Indels
 Score 55; DB 9; I
Pred. No. 0.0034;
 1) Score 55; DB ilarity 100.0%; Pred. No. 0.0 Conservative 0; Mismatches
 1; Mismatches
 CURRENT APPLICATION NUMBER: US/09/730,174A CURRENT FILING DATE: 2000-12-05 NUMBER OF SEQ 1D NOS: 12 SEQ 1D NO 3 LENGTH: 12
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ORGANISM: Artificial Sequence
 ORGANISM: Artificial Sequence
 Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
 ORGANISM: Artificial Sequence
 1 AVSEIQLMHNLG 12
 1 SVSEIOLMHNLG 12
 2 VSEIQLMHNLG 12
 1 VSEIQLMHNLG 11
 Query Match
Best Local Similarity
Matches 11; Conserval
 RESULT 3
US-09-730-174A-1
 US-09-730-174A-3
 SEQ ID NO 1
 SEQ ID NO 6
 TYPE: PRT
 FEATURE:
 FEATURE:
 FEATURE:
 LENGTH
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SEIQLMHN 8
 Query Match
Best Local Similarity
Matches 8; Conserv
 US-10-168-185-8
 US-10-168-185-8
 RESULT 11
US-10-192-673-7
 TYPE: PRT
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 Gaps
 Gaps
 105-10-673-6

Sequence 6, Application US/10192673

Fublication No. US20030166838A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kronenberg, Henry
APPLICANT: Potts, John T.
TITLE OF INVENTION: Bloactive Peptides and Peptide Derivatives of TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
TITLE OF INVENTION: Hormone-Related Peptide (PTHFP)
 ;
 .
0
 78.0%; Score 46; DB 14; Length 10; 90.0%; Pred. No. 0.13; tive 1; Mismatches 0; Indels
 Sequence 1, Application US/10168185
Publication No. US2003017580241
GENERAL INPORMATION:
APPLICANT: Armbruster, Franz Paul
APPLICANT: Armbruster, Franz Paul
APPLICANT: Schmidt-Gayk, Heinrich
APPLICANT: Schmidt-Gayk, Heinrich
APPLICANT: Schmidt-Gayk, Heinrich
APPLICANT: Roth, Heinz-Jurgen
TITLE OF INVENTION: Method for Determining Parathormone
TITLE OF INVENTION: Activity in a Human Sample
FILE REPRENCE: Hiz-04048
CURRENT FILING DATE: 2002-06-17
PRIOR PLICATION NUMBER: US/10/168,185
PRIOR FILING DATE: 2000-12-18
PRIOR FILING DATE: 2000-12-18
PRIOR PLICATION NUMBER: DE 19961350
PRIOR APPLICATION NUMBER: DE 19961350
PRIOR PRIOR OF SEQ ID NOS: 11
SOFTWARE: FastESQ for Windows Version 4.0
 76.3%; Score 45; DB 14; Length 9; 100.0%; Pred. No. 1.2e+06;
 Indels
TITLE OF INVENTION: Activity in a Human Sample FILE REFERENCE: HLZ-004US
CURRENT APPLICATION NUMBER: US/10/168,185
CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: PCT/EP00/12911
PRIOR APPLICATION NUMBER: DE 19961350
PRIOR FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 1
LENGTH: 10
 100.0%; Pred. No.
 Query Match
Best Local Similarity 90.0
Matches 9; Conservative
 Conservative
 1 AVSEIQLMHN 10
 1 SVSEIOLMHN 10
 TYPE: PRT
ORGANISM: Homo sapiens
 2 VSEIQLMHN 10
 ORGANISM: Homo sapiens
 1 VSEIOLMHN 9
 Query Match
Best Local Similarity
Matches 9; Conserv
 -10-168-185-7
 US-10-168-185-1
 US-10-168-185-7
 RESULT 9
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 0
 Gaps
 Gaps
) OTHER INFORMATION: Description of Artificial Sequence: synthetic; CTHER INFORMATION: peptide US-10-192-673-6
 Sequence 7, Application US/10192673
Publication No. US20030166838A1
GENERAL INFORMATION:
APPLICANT: Gardella, Thomas J.
APPLICANT: Kronenberg, Henry
APPLICANT: Potts, John T.
APPLICANT: Dotts, John T.
APPLICANT: Jupponer, Harald
TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
TITLE OF INVENTION: Horantyroid Hormone (PTH) and Parathyroid
TITLE OF INVENTION: Hormone-Related Peptide (PTHP)
 ó
 .;
0
 Sequence 8, Application US/10168185
Publication No. US20030175802A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Armbruster, Franz Paul
APPLICANT: Missbichler, Albert
APPLICANT: Schnidt-Gayk, Heinrich
APPLICANT: Schnidt-Gayk, Heinrich
TITLE OF INVENTION: Method for Determining Parathormone
TITLE OF INVENTION: Activity in a Human Sample
FILE REFERENCE: HIZ-004US
CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: US/10/168,185
CURRENT FILING DATE: 2000-12-18
PRIOR PILING DATE: 2000-12-18
PRIOR FILING DATE: 2000-12-18
PRIOR FILING DATE: 1999-12-17
WUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
 72.9%; Score 43; DB 14; Length 9; 100.0%; Pred. No. 1.2e+06; vative 0; Mismatches 0; Indels
 69.5%; Score 41; DB 14; Length 8; 100.0%; Pred. No. 1.2e+06;
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 0; Mismatches
CURRENT APPLICATION NUMBER: US/10/192,673
CURRENT FILING DATE: 2002-07-11
PRIOR PELICATION NUMBER: U.S. 09/421,379
PRIOR FILING DATE: 1999-10-20
PRIOR APPLICATION NUMBER: U.S. 60/105,530
PRIOR APPLICATION NUMBER: U.S. 60/105,530
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PALENTIN VET: 2.0
SEQ ID NO 6
LENGTH: 9
 ORGANISM: Artificial Sequence
 Query Match 72.9
Best Local Similarity 100.
Matches 9; Conservative
 Conservative
 ORGANISM: Homo sapiens
 1 AVSEIQLMH 9
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 3 SEIQLMHN 10
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```
Hormone-Related Peptide (PTHrP)
TITLE OF INVENTION: Hormone-Related Peptide FILE REFERENCE: 0609-4570002; CURRENT APPLICATION NUMBER: US/10/192,673; CURRENT FILLING DATE: 2002-07-11; PRIOR APPLICATION NUMBER: U.S. 09/421,379; PRIOR FILING DATE: 1999-10-20; PRIOR APPLICATION NUMBER: U.S. 60/105,530; PRIOR FILING DATE: 1998-10-22; NUMBER OF SEQ ID NOS: 13; SEQ ID NO 8; SEQ ID NO 8;
 77.8%;
 TYPE: PRT
ORGANISM: Artificial Sequence
 Query Match 55.9
Best Local Similarity 77.8
Matches 7; Conservative
 Query Match 54.2
Best Local Similarity 87.5
Matches 7; Conservative
 TYPE: PRT
ORGANISM: Homo sapiens
 1 AVSEIQLMH 9
 1 AVSEIQLM 8
 RESULT 15
US-10-192-673-10
 RESULT 14
US-10-168-185-3
 US-10-168-185-3
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0
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 Gaps
 Gaps
 APPLICANT: Gardella, Thomas J.
APPLICANT: Kronenberg, Henry
APPLICANT: Potts, John T.
APPLICANT: Juppiner, Harald
TITLE OF INVENTION: Blackive Peptides and Peptide Derivatives of TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
 OTHER INFORMATION: Description of Artificial Sequence: synthetic; OTHER INFORMATION: peptide US-10-192-673-7
 ..
 67.8%; Score 40; DB 14; Length 9; 88.9%; Pred No. 1.2e+06;
 APPLICANT: Armbrister, Franz Paul
APPLICANT: Amissichler, Albert
APPLICANT: Schmidt-Gayk, Heinrich
APPLICANT: Schmidt-Gayk, Heinrich
APPLICANT: Schmidt-Gayk, Heinrich
TITLE OF INVENTION: Method for Determining Parathormone
TITLE OF INVENTION: Activity in a Human Sample
TITLE OF INVENTION: Activity in a Human Sample
TITLE OF INVENTION: Activity in a Human Sample
TILE REFERENCE: HIZ-00408
CURRENT FILING DATE: 2002-06-17
PRIOR PILING DATE: 2000-12-18
PRIOR PILING DATE: 2000-12-18
PRIOR PILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 11
SOFTMARE: FastSEQ for Windows Version 4.0
 Query Match 67.8%; Score 40; DB 14; Length 9; Best Local Similarity 88.9%; Pred. No. 1.2e+06; Matches 8; Conservative 1; Mismatches 0; Indels
 1; Mismatches
 FILE REFERENCE: 0609.4570002
CURRENT APPLICATION NUMBER: US/10/192,673
CURRENT FILING DATE: 2002-07-11
PRIOR APPLICATION NUMBER: U.S. 09/421,379
PRIOR FILING DATE: 1999-10-20
PRIOR APPLICATION NUMBER: U.S. 60/105,530
PRIOR FILING DATE: 1999-10-22
NUMBER: OF SEQ ID NOS: 13
SEQ ID NO SEQ ID NOS: 20
 ; Sequence 8, Application US/10192673; Publication No. US20030166838A1; GENERAL INFORMATION:
 Sequence 2, Application US/10168185; Publication No. US20030175802A1; GENERAL INFORMATION:
 TYPE: PRT
ORGANISM: Artificial Sequence
 Best Local Similarity 88.9
Matches 8, Conservative
 TYPE: PRT
ORGANISM: Homo sapiens
 1 AVSEIQLMH 9
 SVSEIQLMH 9
 1 AVSEIQLMH 9
 RESULT 13
US-10-192-673-8
 US-10-168-185-2
 Query Match
 SEQ ID NO 2
 CENGTH: 9
 FEATURE:
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Gaps
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 Sequence 10, Application US/10192673
Publication No. US20030166838A1
GENERAL INFORMATION:
APPLICANT: Gardella, Thomas J.
APPLICANT: Fortes, John T.
APPLICANT: Pottes, John T.
APPLICANT: Juppner, Harald
TILE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
FEATURE:
COTHER INFORMATION: Description of Artificial Sequence: synthetic
FEATURE INFORMATION: peptide
15.01-192-673-8
 Sequence 3, Application US/10168185
; Sequence 3, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
 APPLICANT: Armbruster, Franz Paul
; APPLICANT: Armbruster, Franz Paul
; APPLICANT: Schmidt-Gayk, Heinrich
 APPLICANT: Roth, Heinr-Ohren
; TITLE OF INVENTION: Method for Determining Parathormone
; TITLE OF INVENTION: Activity in a Human Sample
; FILE REFERENCE: HLZ-OHGUS
; CURRENT FELING DATE: 2002-06-17
; FRIOR PELLOATION NUMBER: US/10/168,185
; CURRENT FILING DATE: 2000-12-18
; PRIOR FILING DATE: 2000-12-18
; PRIOR FILING DATE: 2000-12-18
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PastSEQ for Windows Version 4.0
; SEQ ID NO 3
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 Score 33; DB 14; Length 9;
Pred. No. 1.2e+06;
1; Mismatches 1; Indels
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66, Appli 67, Appli 271, Appl 75, Appl 10, Appl 10, Appl 107, Appl 71, Appl 71

Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Seq

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US-08-474-140-137A-4-2

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FRATURE:
NAME/KEY: PEPTIDE
LOCATION: (9)
OTHER INFORMATION: H
FRATURE: NAME/KEY: PEPTIDE
 FEATURE:
NAME/KEY: MOD_RES
LOCATION: (8)
OTHER INFORMATION: N
 OTHER INFORMATION:
 Sequence 31, Appli
Sequence 6, Appli
Sequence 7, Appli
Sequence 7, Appli
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Sequence 12, Appli
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Sequence 12, Appli
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6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 US-09-442-989-31

US-08-817-547A-1

US-08-817-547A-2

US-08-817-547A-2

US-08-817-547A-3

US-08-817-547A-3

US-08-817-547A-4

US-08-817-547A-4

US-08-817-547A-14

US-08-817-547A-14

US-08-817-547A-14

US-08-817-547A-14

US-08-817-547A-14

US-08-817-547A-17

US-08-817-547A-17

US-08-817-547A-17

US-08-974-297-64

US-08-817-547A-13

US-08-974-297-64

 Total number of hits satisfying chosen parameters:
 389414 seqs, 51625971 residues
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 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 US-09-730-174A-5
59
1 AVSEIQLMHNLG 12
 Query
Match Length DB
 Minimum DB seq length: 0
Maximum DB seq length: 12
 Title:
Perfect score:
Sequence:
 Scoring table:
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 Searched:
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Result No.

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TYPE: PRT
ORGANISM: Artificial Sequence
 TELECOMMUNE.
TELEBRONG.
TELEBROX: 404-818-3799
TELEBRAX: 404-818-3799
INPORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
TWATH: 9 amino acids
 MOLECULE TYPE: peptide
HYPOTHETICAL: no
 ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 unknown
 1 AVSEIQLMH 9
 1 AVSEIQLMH 9
 CITY: Atlanta
STATE: Georgia
COUNTRY: USA
 ; ANTI-SENSE: no
US-08-817-547A-2
 30303
 US-09-421-379-6
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 Gaps
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 ..
 Score 46; DB 3; Length 10;
Pred. No. 0.019;
1; Mismatches 0; Indels
Score 53; DB 4; Length 12;
Pred. No. 0.0012;
0; Mismatches 1; Indels
 GENERAL INFORMATION:
APPLICANT: Adermann, Knut
APPLICANT: Hock, Dieve, Markus
TITLE OF INVENTION: Peptides from the HFTH Sequence
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS
ADDRESSEE: Jones & Askew, LLP
STREET: 191 Peachtree Street, 37th Floor
 ATREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
CITY: Atlanta
CITY: Atlanta
CITY: Atlanta
CITY: Atlanta
CITY: Atlanta
CITY: 191 Peachtree Street, 37th Floor
CITY: 19303
COMPTTER: 05A
ZIP: 30303
COMPTTER: 13003
COMPTTER: 1300 Compatible
COMPTTER: 1300 COMPATION
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,547A
FILING DATE:
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/03757
FILING DATE: 29 SEPT 1994
ATTORNEY/AGENT INFORMATION:
NAME: FROST, FOGER T.
REGISTRATION NUMBER: 22,176
REFERENCE/DOCKET NUMBER: 07826-0007
TELECOMMUNICATION:
TELEPHONE: 404-818-3799
 Sequence 6, Application US/09421379; Patent No. 6495662; GENERAL INPORMATION: APPLICANT: Gardella, Thomas J.; APPLICANT: Kronenberg, Henry; APPLICANT: Potts, John T.; APPLICANT: Uppner, Harald
 Sequence 1, Application US/08817547A Patent No. 6030790
 89.8%;
91.7%;
 TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 Query Match
Best Local Similarity 90.v
 Query Match
Best Local Similarity 91.7
Matches 11, Conservative
 1 AVSEIQLMHNLG 12
 1 AVSEIQLXHNLG 12
 MOLECULE TYPE: peptide HYPOTHETICAL: no
 1 AVSEIQLMHN 10
 unknown
 TYPE: amino acid STRANDEDNESS: un}
 US-09-421-379-6
 RESULT 3
 엄
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TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid TITLE OF INVENTION: Hormone Related Peptide (PTHrP) rile Derivation (PTHrP) and Parathyroid CURRENT APPLICATION WIMBER: US/09/421,379 CURRENT APPLICATION NUMBER: US, 60/105,530 EARLIER APPLICATION NUMBER: U.S. 60/105,530 NUMBER OF SEQ ID NOS: 13 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 6 LENGTH: 9
 FEATURE: CTHER INFORMATION: Description of Artificial Sequence: synthetic CTHER INFORMATION: peptide
 Score 43; DB 4; Length >; Pred, No. 3e+05; 0; Indels
 Sequence 2, Application US/08817547A;
Sequence 2, Application US/08817547A;
Sequence 2, Application US/08817547A;
Sequence 2, Application;
GENERAL INFORMATION:
APPLICANT: Hock, Dieter;
APPLICANT: Hock, Dieter;
APPLICANT: Maceriain, Markus
TITLE OF INVENTION: Peptides from the hPTH Sequence;
CORRESPONDENCE 3.5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew, LLP
STREET: 191 Peachtree Street, 37th Floor
 MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTING Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/817,547A FILING DATE:
 Query Match 72.9%; Score 43; DB Best Local Similarity 100.0%; Pred. No. 3e+ Matches 9; Conservative 0; Mismatches
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/03757
FILING DATE: 29 SEPT 1994
ATTORNEY/AGENT IRFORMATION:
NAME: FROST, ROGER T.
REGISTRATION NUMBER: 22,176
REFERENCE/DOCKET NUMBER: 07826-0007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
```

; 0

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1 AVSEHQLEHN 10
 1 AVSEIQLMH 9
 1 AVSEHOLLH 9
 RESULT 8
US-08-817-547A-3
 à
 ;
0
 0
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 Gaps
 Gaps
 APPLICANT: Gardella, Thomas J.
APPLICANT: Gardella, Thomas J.
APPLICANT: Gardella, Thomas J.
APPLICANT: Stonenberg, Henry
APPLICANT: Uppner, Harald
TITLE OF INVENTION: Bloactive Peptides and Peptide Derivatives of
TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)
FILE REFERENCE: 0609.4570001
CURRENT APPLICATION NUMBER: US/09/421,379
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: U.S. 60/105,530
EARLIER FILING DATE: 1998-10-22
NUMBER OF SEQ ID NOS: 13
 OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: peptide
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 Score 35, DB 6, Length 11;
Pred. No. 2.2;
0; Mismatches 2; Indels
 67.8%; Score 40; DB 3; Length 9;
88.9%; Pred. No. 3e+05;
tive 1; Mismatches 0; Indels
 DB 4; Length 9; 3e+05;
 PACENT NO. 5460978

PACENT NO. 5460978

PROCE E. WETTENHALL, RICHARD E.H.

TITLE OF INVENTION: PROTEIN ACTIVE IN HÜMORAL

HYPERCALCEMIA OF MALIGNANCY-PTHRP

CURRENT APPLICATION DATA:

PRIOR APPLICATION NUMBER: US/07/715,280

FILING DATE: 14-JUN-1991

PRIOR APPLICATION NUMBER: 199,235

FILING DATE: 09-MAY-1988

APPLICATION NUMBER:
 1; Mismatches
 67.8%; Score 40;
88.9%; Pred. No.
 Sequence 7, Application US/09421379
Patent No. 6495662
GENERAL INFORMATION:
 Query Match
Best Local Similarity 80.0%;
Matches 8; Conservative
 TYPE: PRT ORGANISM: Artificial Sequence
 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO.7
 Query Match
Best Local Similarity 88.9
Matches 8; Conservative
 Best_Local Similarity 88.5
Matches 8; Conservative
 1 AVSEIQLMH 9
 FILING DATE:
 SEQ ID NO:3:
 US-09-421-379-7
 Query Match
 RESULT 6
5460978-3
 5460978-3
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1 AVSEIQLMHN 10

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WESULT 7

WESULT 7

WESULT 7

WESULT 7

WESULT 8

WESULT
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us-09-730-174a-5.closed.rai

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30303
 STATE: N
 COUNTRY:
 Matches
 g
 δ
 ö
 Gaps
 Gaps
 Sequence 10, Application US/09421379;
Patent No. 649562;
GENBRAL INFORMATION:
APPLICANT: Gardella, Thomas J.
APPLICANT: Harald
ITTLE OF INVENTION: Beactive Peptides and Peptide Derivatives of
ITTLE OF INVENTION: Hormone-Related Peptide (PTHF)
ITTLE OF INVENTION: Hormone-Related Peptide (PTHF)
ITTLE OF INVENTION: Hormone-Related Peptide (PTHF)
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: U.S. 60/105,530
EARLIER FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic; OTHER INFORMATION: peptide
US-09-421-379-10
 .
0
 Sequence 4, Application US/08817547A

Patent No. 6030790

GENERAL INFORMATION:

APPLICANT: Adermann, Knut
APPLICANT: Magerlein, Markus

ITLE OF INVENTION: Peptides from the hPTH Sequence
NUMBER OF SEQUENCES: 36

CORRESPONDENCE ABNEW, LLP

STREET: 191 Peachtree Street, 37th Floor
 1; Indels
 0; Indels
 Score 30; DB 4; Length 9;
Pred. No. 3e+05;
 Length 8;
 2; Mismatches
 1; Mismatches
 Score 32;
Pred. No:
 54.2%;
 50.8%;
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
 ORGANISM: Artificial Sequence
 Query Match
Best Local Similarity 66.7
Matches 6; Conservative
 Ouery Match
Best Local Similarity 87.5
Matches 7, Conservative
 SS: unknown unknown
 MOLECULE TYPE: peptide
; HYPOTHETICAL: no
ANTI-SENSE: no
US-08-817-547A-3
 1 AVSEIQLMH 9
 SVSEHOLLH 9
 TYPE: amino acid
STRANDEDNESS: unk
TOPOLOGY: unknown
 1 AVSEIQLM 8
 1 SVSEIQLM 8
 CITY: Atlanta
 RESULT 9
US-09-421-379-10
 RESULT 10
US-08-817-547A-4
 TYPE: PRT
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Gaps
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 COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: ISM PC compatible

COMPUTER: ISM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/428,257A

FILING DATE: 07/05/95

CLASSIFICATION: 514
 45.8%; Score 27; DB 3; Length 7; 85.7%; Pred. No. 3e+05;
 Indels
CAPPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Parent Procession #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,547A
FILING DATE:
PRIOR APPLICATION NUMBER: PCT/EP95/03757
FILING DATE: 29 SEPT 1994
ATTORNEY/AGENT INFORMATION:
NAME: FROST, ROGER T.
REGISCHALTON NUMBER: 22,176
REFERENCE/DOCKET UNMBER: 22,176
REFERENCE/DOCKET UNMBER: 22,176
 APPLICANT: Spooner, Robert A.
APPLICANT: Spooner, A.A.
TITLE OF INVENTION: Compounds to target cells
TITLE OF INVENTION: Compounds to target cells
CORRESPONDENCES: 80
CORRESPENCE ADDRESS:
ADDRESSEE: Jules E. Goldberg
STREET: 261 Madison Avenue
STREET: New York
STATE: NY
 US-08-428-257A-14
; Sequence 14, Application US/08428257A
Patent No. 5885808
; GENERAL INFORMATION:
 TELECOMMUNICATION INFORMATION
TELEPRAX: 404-818-3700
TELERAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
 INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS:
 10 amino acids
 6; Conservative
 SS: unknown
unknown
 SIGNATURE TYPE: unknown
MOLECULE TYPE: peptide
 TYPE: amino acid sTRANDEDNESS: unl
 amino acid
 Query Match
Best Local Similarity
 1 AVSEIOL 7
 1 SVSEIQL 7
 HYPOTHETICAL: n

ANTI-SENSE: no

US-08-817-547A-4
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Gaps
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0
 Score 24; DB 2; Length 5;
Pred. No. 3e+05;
2; Mismatches 0; Indels
 Sequence 56, Application US/08687706
Patent No. 5928892
INFORMATION:
TILLE OF INVENTION:
MUMBER OF SEQUENCES:
CORRESPONDENCES:
CORRESPONDENCES:
ADDRESSE:
Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STREET: WAR
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,706
FLING DATE: 26-JUU-1996
FLING DATE: 26-JUU-1996
FLING DATE: 26-JUU-1996
FILING DATE: 26-JUU-1996
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STREET: 4800 One Atlantic Center
CITY: Atlanta
CITY: Atlanta
STREET: 4800 One Atlantic Center
CITY: Atlanta
STREET: 4800 One Atlantic
COUNTRY: Georgia
CONDUTER: Georgia
CONDUTER: BEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BAR PC COMPATION
MEDIUM TYPE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/177,109A
FILING DATE: 03-JAN-1994
CLASSIFICATION NUMBER: 31,284
ATTORNEY/AGENT INFORMATION:
MAME: Pabst, Patrea
NAME: Pabst, Patrea
TELEFONMUNICATION INFORMATION:
TELEFONMUNICATION NUMBER: 31,284
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/177,109
FILING DATE: 03-JAN-1994
CLASSIFICATION: 514
 40.7%;
 ATTORNEY/AGENT INFORMATION:
 Query Match
Best Local Similarity 60.0
Matches 3; Conservative
 Pabst, Patrea L
 MOLECULE TYPE: protein HYPOTHETICAL: NO
 8 MHNLG 12
 1 LHNMG 5
 JS-08-687-706-56
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 g
 APPLICANT: Komoriya, Akira
APPLICANT: Receive Beverly S.
APPLICANT: Packard, Beverly S.
TITLE OF INVENTION: Compositions for the Detection of Enzyme
TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
NUMBER OF SEQUENCES:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
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 Gaps
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 Score 25; DB 2; Length 10;
Pred. No. 1.4e+02;
1; Mismatches 0; Indels
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Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels
 STATE: CALLLOLLE
COUNTRY: USA

ZIP: 94111-3834

ZIP: 94111-3834

COMPUTER READABLE FORM:
REDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/802,981
FILING DATE: 20-FEB-1997
CLASSIFICATION 1435
ATTORNEY/ARDAT INFORMATION:
NAME: HOLLEY, TOM
REGISTRATION NUMBER: 38,498
REGISTRATION NUMBER: 18,498
REJECHOME (415) 576-0200
TELECOMMUNICATION INFORMATION:
TELEBHONE: (415) 576-0200
TELEFRAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 124:
SEQUENCE CHARACTERISTICS:
TENTH: 11 amino acids
 Sequence 56, Application US/08177109A
Patent No. 5869615
GENERAL INFORMATION:
APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby
TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES
NUMBER OF SEQUENCES: 62
 ; LOCATION: 3
; OTHER INFORMATION: /product= "Aib"
US-08-802-981-124
 RESULT 12
US-08-802-981-124
Sequence 124, Application US/08802981
Patent No. 6037137
GENERAL INFORMATION:
 42.4%;
 NAME/KEY: Modified-site
 Query Match
Best Local Similarity 83.3
Matches 5; Conservative
 TOPOLOGY: linear MOLECULE TYPE: peptide
 STREET: Two Embarcad
CITY: San Francisco
STATE: California
 TYPE: amino acid STRANDEDNESS:
 |||:||
4 VSEVQL 9
 6 QLMHN 10
 5 OLLHN 9
 US-08-177-109A-56
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 0; Gaps
 0;
 Query Match
40.7%; Score 24; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels
 40.7%; Score 24; DB 2; Length 5; 60.0%; Pred. No. 3e+05; tive 2; Mismatches 0; Indels
 RESULT 15
US-08-817-547A-17
i Sequence 17, Application US/08817547A
patent No. 6030790
j Patent No. 6030790
j Patent Nor. 603070
j Patent Nor. 603070
j Patent Nor. 603070007
j Patent Nor. 603070000
 TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
; LENGTH: 5 amino acids; TYPE: amino acid; TOPOLOGY: linear; NOLECULE TYPE: protein; HYPOTHETICAL: NO US-08-687-706-56
 Query Match
Best Local Similarity 60.0
Matches 3; Conservative
 TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
 MOLECULE TYPE: peptide HYPOTHETICAL: no
 8 MHNLG 12
 :||:|
1 LHNMG 5
 HYPOTHETICAL: n
HATI-SENSE: no
US-08-817-547A-17
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Search completed: September 5, 2004, 09:38:33 Job time : 11 secs
 à
REGISTRATION NUMBER: 31,284
REFERNEE/GOCKET NUMBER: WU 107 DIV
TELEPHONE: (404) 873-8794
TELEPHONE: (404) 873-8795
TELEPHONE: (404) 873-8795
INFORMATION FOR SEQ ID NO: 56: SEQUENCE CHARACTERISTICS:
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

September 5, 2004, 09:30:43; Search time 9.5 Seconds (without alignments) 121.505 Million cell updates/sec Run on:

US-09-730-174A-6 61 1 AVSEIQFMHNLG 12

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 12

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

|            |        |           | ochrome b559 | epto   | in UI49 - | l protei | 7      | T-cell receptor al | europeptide M-I | Id heavy chain Cr | locustamyotropin - | Iq heavy chain V r | T-cell receptor al | lpha-myosin hea | hypertrehalosemic | hypertrehalosemic | amine oxidase (con | polyphosphate-gluc | Id heavy chain CDR | N-methylpurine DNA |        | lectin GNL1 alpha | -cell  | hodopsin homolo | 5-aminoimidazole_r |        | T-cell receptor be | eptide Ant | ribosomal protein | hypertrehalosemic | adipokinetic hormo |
|------------|--------|-----------|--------------|--------|-----------|----------|--------|--------------------|-----------------|-------------------|--------------------|--------------------|--------------------|-----------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------|-------------------|--------|-----------------|--------------------|--------|--------------------|------------|-------------------|-------------------|--------------------|
| CONTRACTOR |        | QI        | 2805         | PH1187 | 71        | S78420   | A60589 | PH1190             | A05169          |                   | A43975             | S21205             | PH1189             | 146868          | JC1416            | 809138            | A32428             | S29735             | PT0231             | A56029             | S33844 | S38304            | E49033 | ന               | 33                 | PH1174 | S51737             | A35779     | 7802              | S08995            | 4982               |
|            |        | Length DB |              |        |           |          |        | 2                  | æ               | 0                 | N                  |                    | N                  |                 | 0                 |                   |                    |                    |                    |                    | 0      |                   | 0      | -               |                    |        |                    |            |                   | 89                |                    |
| 9/0        | Query  | - !       | 32.8         | 'n.    | σ,        | ď        | ď      | ď                  | 7               | ۲.                | ζ.                 | ζ.                 | ζ.                 | ů.              | Ġ                 | ú                 | 'n                 | 4.                 | ₹.                 | 4.                 | 4.     | 4.                | 4.     | 4.              | 4.                 | 4.     | ₩.                 | ά.         | w.                | 23.0              | m.                 |
|            |        | Score     | 20           | 20     | 18        | ,18      | 18     | 18                 | 17              | 17                | 17                 | 17                 | 17                 | 16              | 16                | 16                | 16                 | 15                 | 15                 | 15                 | 15     | 15                | 15     | 15              | 15                 | 15     | 15                 | 14         | 14                | 14                | 14                 |
|            | Result | No.       |              | 7      | m         | 4        | Ŋ      | ω                  | 7               | œ                 | σı                 | 10                 | 11                 | 12              | 13                | 14                | 15                 | 16                 | 17                 | 18                 | 19     | 20                | 21     | 22              | 23                 | 24     | 25                 | 56         | 27                | 28                | 20                 |

| neuropeptide Led-C<br>chlorophyll a/b-bi | ·H                                             | nypounetical proce<br>ranatachykinin C -<br>e anticen n20e pre | alliFMRFamide<br>ranslation ele | endo-1,4-beta-xyla<br>protein QA300042 | retinal oxidase -<br>beta-D-galactosida | transcription fact potB protein - Sal | T-cell receptor al |
|------------------------------------------|------------------------------------------------|----------------------------------------------------------------|---------------------------------|----------------------------------------|-----------------------------------------|---------------------------------------|--------------------|
| A44960<br>PW0002                         | PT0238<br>SPPGNK                               | C61033<br>B46453                                               | C44787<br>B41835                | S19301<br>PA0028                       | S60354<br>S53436                        | S25485<br>S71034                      | PH1175             |
| 0.0                                      | 01 H C                                         | 100                                                            | 0 0                             | 2 2                                    | N N                                     | ~ ~                                   | 0                  |
| <b>ω</b> σν -                            | 016                                            | 201                                                            | 10                              | 11                                     | 11 11                                   | 12                                    | 12                 |
| 23.0                                     | 23.00                                          | 23.0                                                           | 23.0                            | 23.0                                   | 23.0                                    | 23.0                                  | 23.0               |
| 4 T                                      | 444                                            | 1 T T                                                          | 1 4                             | 14                                     | 14                                      | 다 다<br>주 주                            | 14                 |
| 30                                       | 3 3 4<br>2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 | 333                                                            | 3.7<br>3.8                      | 3.9<br>4.0                             | 4. 4.<br>1. 2.                          | 4.4<br>6.4                            | <b>4</b>           |

# ALIGNMENTS

| 8055                          |          |                |     |       |   |          |                   |         |
|-------------------------------|----------|----------------|-----|-------|---|----------|-------------------|---------|
| rtochrome                     | ome b559 | component psbF | int | psbF  | i | pepper   | epper chloroplast | (fragme |
| Species: chloroplast Capsicum | chlo     | roplast        | Car | sicum | Ø | annunm ( | (pepper)          | 1       |

RESULT 1
\$28055
cytochrome b559 component psbF - pepper chloroplast (fragment)
C;Species: chloroplast Capsicum annuum (pepper)
C;Species: chloroplast Capsicum annuum (pepper)
C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 11-Jun-1999
C;Accession: \$28055 B. Weil, J.H.; Schantz, R.
R;Kuntz, M.; Camara, B.; Weil, J.H.; Schantz, R.
R;Kuntz, M.; Camara, B.; Weil, J.H.; Schantz, R.
R;Kuntz, M.; Camara, B.; Weil, J.H.; Schantz, R.
A;Rute: The psbb. gene from bell pepper (Capsicum annuum): plastid RNA editing also occ:
A;Reference number: \$28055; MUID:93099270; PMID:1463853
A;Accession: \$28055
A;Molecule type: DNA
A;Residues: L-10 «KUNA
A;Residues: L-10 «KUNA
A;Cross-references: EMBL:X65570; NID:g14344; PIDN:CAA46539.1; PID:g415734
C;Genetics: psbF
A;Genetics
C;Superfamily: cytochrome b559 component F
C;Superfamily: cytochrome b559 component F
C;Superfamily: cytochrome b559 component F
C;Keywords: chloroplast; photosynthesis; photosystem II; thylakoid

Gaps .. 0 Query Match 32.8%; Score 20; DB 2; Length 10; Best Local Similarity 37.5%; Pred. No. 7.4e+02; Matches 3; Conservative 4; Mismatches 1; Indels

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1 AVSEIQFM 8 1 SISAMOFI 8 ò g

T-cell receptor alpha chain V region (Cw3/1F11) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 16-Ju1-1999 #sequence\_revision 16-Ju1-1999 #text\_change 16-Ju1-1999
C;Accession: PH1187
R;Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wi. J. Exp. Med. 176, 439-447, 1992
A;Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell recepto A;Reference number: 226512; MUID:92364546; PMID:1380061
A;Accession: PH1187
A;Accession: PH1187
A;Accession: PH1187
A;Accession: PH1187
A;Accession: PH1187
A;Residues: 1-12 cCAS>

.; 0 Score 20; DB 2; Length 12; Pred. No. 9.1e+02; 0; Mismatches 2; Indels Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative 0

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T-cell receptor alpha chain V region (Cw3/10.1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C;Datesion: PH1190
R;Casanova, J.L; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid J. Exp. Med. 176, 439-447, 1992
J. Exp. Med. 176, 439-447, 1992
A;Title: H.2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor A;Reference number: $26512; MJID:92364546; PMID:1380061
 is heavy chain C region (129) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 13-Mar-1998
C;Accession: A37268
R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
A; Biol. Chem. 266, 6607-6613, 1991
A;Title: Heavy and light chain variable region sequences and antibody properties of antiba; A;Reference number: A38740; MUID:91177923; PMID:1706720
 C)Accession: A05169
R)Witten, J.L.; Schaffer, M.H.; O'Shea, M.; Cook, J.C.; Hemling, M.E.; Rinehart Jr., K.L. Biothem. Blobhys. Res. Comunn. 124, 350-358, 1984
A;Title: Structures of two cockroach neuropeptides assigned by fast atom bombardment mas A;Reference number: A90118; MUID:85046530; PMID:6548628
A;Accession: A05169
A;Molecule type: protein
A;Residues: 1-8 <WIT>
C;Keywords: neuropeptide
 neuropeptide M-I - American cockroach
C,Species: Periplaneta americana (American cockroach)
C,Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 31-Dec-1993
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 Score 18; DB 2; Length 12; Pred. No. 2.3e+03; 0; Mismatches 2; Indels
 Length 10;
 Score 17; DB 2; Length 8; Pred. No. 2.8e+05; indels 1; Mismatches 3; Indels
 4; Indels
 27.9%; Score 17; DB 2; I 44.4%; Pred. No. 2.9e+03; ative 1; Mismatches 4;
 27.9%;
 29.5%;
 Query Match
Best Local Similarity 44.4.
 Query Match
Best Local Similarity 42.9
Matches 3; Conservative
 5; Conservative
 4 EIQFMHNLG 12
 1 ESÓSFPNVG 9
 4 EIQFMHN 10
 1 EVNFSPN 7
 Query Match
Best Local Similarity
Matches 5; Conserv
 1 AVSEIQF 7
 2 AVSENGF 8
 A,Accession: A37268
A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-10 <RUF>
 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-12 <CAS>
 RESULT 8
 A37268
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 sperm-activating peptide (Tyr-2, Asn-3, Gly-5, Ile-9, Asp-10 SAP-I) - slate-pencil urching sperm-activating peptide (Tyr-2, Asn-3, Gly-5, Ile-9, Asp-10 SAP-I) - slate-pencil urching Species: Heterocentrotus mamillatus
C;Species: Heterocentrotus mamillatus
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
C;Accession: A60589
R;Yoshino, K.I.; Kajiura, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguc Comp. Biochem. Physiol. B 94, 739-751, 1989
Comp. Biochem. Physiol. B 94, 739-751, 1989
Comp. Biochem. Physiol. B 94, 739-751, 1989
Cours undus, Echinometra mathaei and Heterocentrotus mammillatus.
A;Reference number: A60527
A;Accession: A60589

 C;Species: Carnobacterium sp.
C;Species: Carnobacterium sp.
C;Date: 23-Jan-1998 #sequence_revision 30-Jan-1998 #text_change 30-Jan-1998
C;Accession: A58718
R;Stoffels, G: Nissen-Meyer, J:; Gudmundsdottir, A.; Sletten, K.; Holo, H.; Nes, I.F.
Appl. Environ. Microbiol. 58, 1477-1422, 1992
A;Title: Purification and characterization of a new bacteriocin isolated from a Carnobac A;Reference number: A58718; MUID:92321768; PMID:1622206
A;Reference number: protein
A;Residues: protein
A;Residues: 1-7 <5TO.
C;Keywords: antibiotic; lanthionine
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 Cibosomal protein RL41, mitochondrial [validated] - rat (fragment)
CiSpecies: Rattus norvegicus (Norway rat)
CiSpecies: Rattus norvegicus (Norway rat)
CiSpecies: Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jul-2000
CiAccession: S74420
R;Goldschmidt-Reisin, S.; Graack, H.R.
Submitted to the Protein Sequence Database, February 1998
A;Reference number: S78410
A;Recession: S78420
A;Molecule type: protein
A;Residues: 1-9 GGDL>
A;Note: the protein is designated as mitochondrial ribosomal protein L41
C;Keywords: mitochondrion; protein biosynthesis; ribosome
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 29.5%; Score 18; DB 2; Length 10; ilarity 75.0%; Pred. No. 1.8e+03; Conservative 1; Mismatches 0; Indels
 29.5%; Score 18; DB 2; Length 9; ilarity 75.0%; Pred. No. 2.8e+05; Conservative 0; Mismatches 1; Indels
 Length 7;
 29.5%; Score 18; DB 2; Le
100.0%; Pred. No. 2.8e+05;
tive 0; Mismatches 0;
 carnocin UI49 - Carnobacterium sp. (fragment)
 4; Conservative
 Query Match
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3; Conserve
 Query Match
Best Local Similarity
Matches 3; Conserv
 Query Match
Best Local Similarity
Matches 4; Conserv
 9 HNLG 12
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2 YNLG 5
 HNLG 12
 3 SEIQ 6
 HRLG 8
 SEIQ 5
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Gaps

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C;Species: Caracisius morosus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: d11416; 807157; 807157
R;Gaede, G; Xellner, R:; Rinehart, K.L.; Proefke, M.L.
R;Gaede, G; Xellner, Res. Commun. 189, 1303-1309, 1992
A;Title: A tryptophan-substituted member of the AKH/RPCH family isolated from a stick ir A;Reference number: J01416; MUID:93129188; PMID:1482345
 A,Molecule type: protein
A,Residues: 1-10 GABI>
K,Gaede, G., Rinehart Jr., K.L.
Biol. Chem. Hoppe-Seyler 368, 67-75, 1987
A,Title: Primary structure of the hypertrehalosaemic factor II from the corpus cardiacum
A,Reference number: S07157; MUID:87157103; PMID:3828078
 A; Molecule type: protein.
A; Residues: '2', 2-10 < GA32>
C; Comment: Hypertrehalosemic factor II lacks the tryptophan modification.
C; Comment: This peptide raises hemolymph levels of trehalose in the cockroach Periplane C; Superfamily: adipokinetic hormone
C; Superfamily: adipokinetic hormone
C; Superfamily: adipokinetic hormone
F; Hydrodidiae and action and action action action action and action action and action ac
 rabbit alpha- and beta-ventricul
 C.Species: Oryctolagus cuniculus (domestic rabbit)
C.Species: Oryctolagus cuniculus (domestic rabbit)
C.Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 05-Nov-1999
C.Accession: 146684, P.K.; Sinha, A.M.; Hsu, H.
Proc. Natl. Acad. Sci. U.S.A. 81, 3044-3048, 1984
A.Fitla: Characterization of genomic clones specifying rabbit alpha- and bet A.Reference number: 146868; MUID:84221901; PMID:6328491
 A;Status: preliminary; translated from GB/EMBL/DDBJ
*Molecule type: DNA
A;Residues: 1-7 <FRI>A;Cross-references: GB:K01698; NID:g165538; PIDN:AAA31415.1; PID:g165539
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 (Carausius morosus)
Indels
 Indels
 Length 7;
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 26.2%; Score 16; DB 2; I 60.0%; Pred. No. 2.8e+05; iive 1; Mismatches 1;
Mismatches
 stick insect
le Cam-HrTH-I
 hypertrehalosemic hormone I - stick inse
N;Alternate names: neuropeptide Cam-HrTF
N;Contains: hypertrehalosemic factor II
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0
 Conservative
Conservative
 12
 alpha-myosin heavy chain
 4 EIQFMHNLG
 1 OLTFTPNWG
 Query Match
Best Local Similarity
 6 OFMHN 10
 OKMHD 5
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 C.Species: Homo sapiens (man, C.Species: Homo sapiens (man, C.Species: Homo sapiens (man, C.Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_cnange ro-rays c.Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_cnange ro-rays c.Speciesion: 221205 R;Maxiya, R.; Stigbrand, T. Bur. J. Biochem. 205, 341-345, 1992 A.Title: Placental alkaline phosphatase has a binding site for the human immunoglobulin-A;Reference number: 821205, MUID:92209522; PMID:155592 A.Accession: 821205 A.Ac
 Treal receptor alpha chain V region (Cw3/2C3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 16-Ju1-1999 #sequence_revision 16-Ju1-1999 #text_change 16-Ju1-1999
C;Accession: PH189
R;Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
A;Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor A;Reference number: S26512; MUID:92364546; PMID:1380061
A;Accession: PH189
A;Accession: PH189
A;Accession: PH189
A;Accession: PH189
A;Accession: PH189
A;Accession: PH189
 NyAlternate names: Low-WT
Cyberies: Low-WT
A;Title: Isolation, identification and synthesis of locustamyotropin (Low-MT), a novel had the reference number: A43975; MUD:90341077; PMID:1974346
A;Accession: A43975; MUD:90341077; PMID:1974346
A;Accession: A43975
A;Accession: A43977
A;Accession: A43977
A;Accession: A43977
A;Accession: A43977
A
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 g heavy chain V region - human
Species: Homo sapiens (man)
Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
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 Query Match 27.9%; Score 17; DB 2; Length 12; Best Local Similarity 33.3%; Pred. No. 3.5e+03; Matches 3; Conservative 3; Mismatches 3; Indels
 Length 12;
 DB 2; Le
3.5e+03;
 Score 17;
Pred. No.
 ocustamyotropin - migratory locust
Alternate names: Lom-MT
 27.9%; 2
 1 AVSEIQFMHNL 11
 2 AVPAAOFSPRL 12
 4 EIQFMHNLG 12
 |:| : |
EVQLVESGG 9
 Query Match
Best Local Similarity
 Status: preliminary
Molecule type: mRNA
Residues: 1-12 <CAS>
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Rivan der Meer, R. A.; van Wassenaar, P.D.; van Brouwershaven, J.H.; Duine, J.A. Blochen. Blo
 A, Accession: S0918
A, Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: notein
A; Molecule type: notein
A; Molecule type: notein the maino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have C; Superfamily: adipokinetic hormone
C; Superfamily: adipokinetic hormone
F; Meywords: amidated carboxyl and hormone; neuropeptide; pyroglutamic acid
F; Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F; 10/Modified site: amidated carboxyl end (Thr) #status experimental
 isolated from the corpor
tandem fast atom bombard
hypertrehalosemic hormone II - stick insect (Extatosoma tiaratum)
Nalternate names: Cam-HTTH-II
C;Specias: Extatosoma tiaratum
C;Space: 30-Jun-1992 #sequence_revision 24-Oct-1997 #text_change 31-Oct-1997
C;Accession: S09138
G;Accession: S09138
G;Accession: K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A;Pitle: Parinary structures of hypertrehalosamic neuropeptides isolated froentals and of the stick insect Extatosoma tiaratum assigned by tandem fast
A;Reference number: S08995; MUID:90253659; PMID:2340112
 amine oxidase (copper-containing) (EC 1.4.3.6) - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 12-Oct-1989 #sequence_revision 31-Dec-1993 #text_change 06-Sep-1996
C;Accession: A32428
 Gaps
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 Length 11;
 Length 10;
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26.2%; Score 16; DB 2; Length 10;
Best Local Similarity 33.3%; Pred. No. 4.5e+03;
Matches 3; Conservative 2; Mismatches 4; Indels
 3; Indels
 Score 16; DB 2;
Pred. No. 5e+03;
2; Mismatches
 5, 2004, 09:37:44
 26.2%;
 3; Conservative
 Search completed: September
Job time : 9.5 secs
 4 EIQFMHNLG 12
 1 OLTFTPNWG 9
 3 SEIQFMHN 10
 2 SDAVFIYN 9
 Query Match
Best Local Similarity
 RESULT 15
A32428
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Gaps

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

September 5, 2004, 09:27:07; Search time 6.5 Seconds (without alignments) 96.130 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-730-174A-6 61 1 AVSEIQFMHNLG 12

Scoring table:

141681 segs, 52070155 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

501 Total number of hits satisfying chosen parameters:

Minimum DB\seq length: 0 Maximum DB seq length: 12

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

|            | otion       |            | U      |        |        | cydia po |        |         |        |           |        |        |        |            |        |        |        |        |            | carcinus ma |            |            | ran    | S      |            |        |        |        |        |        | Ч      |            |        | eisenia foe  |
|------------|-------------|------------|--------|--------|--------|----------|--------|---------|--------|-----------|--------|--------|--------|------------|--------|--------|--------|--------|------------|-------------|------------|------------|--------|--------|------------|--------|--------|--------|--------|--------|--------|------------|--------|--------------|
|            | Description | 003367     | P36960 | P18110 | P22395 | P82157   | P11385 | P82099  | P81010 | P81350    | P49820 | P58707 | P82158 | P82065     | P81821 | P82152 | P04548 | P83281 | P38640     | P81822      | P83317     | P41867     | P22690 | P01292 | P83146     | P80903 | 056251 | P36414 | P25419 | P21143 | P19988 | P05486     | P19852 | P42998       |
|            |             |            |        |        |        |          |        |         |        |           |        |        |        |            |        |        |        |        |            |             |            |            |        |        |            |        |        |        |        |        |        |            |        |              |
| n          |             |            |        |        |        |          |        |         |        |           |        |        |        |            |        |        |        |        |            |             |            |            |        |        |            |        |        |        |        |        |        |            |        |              |
|            | 1           | PSBF_CAPAN | CARUI  | ROMMI  | LOCMI  |          | CARMO  | 3_LITRU | FUSSO  | EFG CLOPA | CANFA  | ANTEL  | CYDPO  | TY51_LITRU | CARMA  | CYDPO  | PERAM  | MACRS  | UF02_MOUSE | CARMA       | FAR2_PENMO | FARC CALVO | RANCA  | . PIG  | ASL1_BACSE |        |        | PSEPU  | TENMO  | LEUMA  | LEUMA  | ł          | CLYJA  | _EISFO       |
| •          | 10          | PSBF       | LANC   | HTF1   | LMT    | ALL6     | HTF2   | EI03    | FUSSE  | EFG       | NUHIM  | FLRN   | ALL7_C | TY51       | AL18   | ALL1   | HTF1   | FAR8   | UF02       | AL19        | FARS       | FARC       | TKNC   | TKNK   | ASL1       | PORD   | RS19   |        | HTF    | LCK4   | LCK6   | ONO<br>ONO | MOSH   | OXYT         |
| 1          | DB<br>      | Н          | Н      | rH     | Н      | Н        | тd     | Н       | Н      | Н         | Н      | Н      | Н      | Н          | Н      | Н      | гH     | Н      | -1         | Н           | Н          | Н          | Н      | ٦      | Н          |        | н      | н      | г      | н      | Н      | Н          | Н      | <del>-</del> |
|            | Length      | 10         | 7      | 10     | 12     | മാ       | 10     | ŧ۸      | æ      | 11        | 11     | 4      | 7      | 7          | Φ      | œ      | ထ      | σn     | σ          | 10          | 10         | 10         | 10     | 10     | 11         | 12     | 12     | 9      | 00     | ω      | ∞      | σ          | o.     | σ            |
|            | - 1         | •          | •      | •      | •      | •        | •      | •       | •      |           | •      | •      | •      |            | •      | •      | •      | •      | •          | •           | •          | ٠          | •      | •      | •          | •      | •      | •      | •      | •      | ٠      | •          | 'n     | m.           |
| %<br>Query | Match       | 32         | 5      | 23     | 27     | 26       | 26     | 24      | 24     | 24        | 24     | 23     | 23     | 23         | 23     | 23     | 23     | 23     | 23         | 23          | 23         | 23         | 23     | 23     | 23         | 23     | 23     | 2      | 21     | 2      | 2      | 21         | 2      | 21           |
| ·          | Score       | 20         | 18     | 18     | 17     | 16       | 16     | 15      | 15     | 15        | 15     | 14     | 14     | 14         | 14     | 14     | 14     | 14     | 14         | 14          | 14         | 14         | 14     | 14     | 14         | 14     | 14     | 13     | 13     | 13     | 13     | 13         | 13     | 13           |
| Result     | NO.         | Н          | 7      | m      | 4      | ស        | φ      | 7       | 80     | σ         | 10     | 11     | 13     | 13         | 14     | 15     | 16     | 17     | <b>8</b> 0 | 19          | 20         | 21         | 22     | 23     | 24         | 25     | 56     | 27     | 28     | 29     | 30     | 31         | 32     | 33           |

| P82691 periplaneta P83147 bacteroides P1145 periplaneta P81095 bacillus su P41837 periplaneta P8046 comamonas t P31144 homo sapien P82071 litoria rub Q10582 bethrops ja Q10582 bethrops ja P04549 periplaneta P19346 erythrocebu |  |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--|
| 9 1 PPK1 PERAM<br>111 1 AS12_BACSE<br>111 1 CONZ_PERAM<br>111 1 CS15_BACSU<br>111 1 QCAC_COMPE<br>111 1 QCAC_COMPE<br>12 1 UKA2_HUAN<br>5 1 RE21_LITRU<br>5 1 RE21_LITRU<br>8 1 ANG2_BOTUA<br>8 1 HTF2_PERAM<br>9 1 FIBB_ERXPA    |  |
| 13 21.3<br>13 21.3<br>13 21.3<br>13 21.3<br>12 21.3<br>12 21.3<br>19.7<br>19.7<br>19.7                                                                                                                                            |  |
| и ш ш ш ш ш ц ц ц ц ц ц ц ц ц ц ц ц ц ц                                                                                                                                                                                           |  |

# ALIGNMENTS

Mismatches .∵ 3; Conservative 1 AVSEIQFM 8 :: | : | : | 1 SISAMQFI 8 Matches à

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 TESCHE-Corpora cardiaca;

RX TESCHE-Corpora cardiaca;

RX Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;

RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;

RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from research analyses of two neuropeptides of the AKH/RPCH-family from The lubber grasshopper, Romalea microptera.";

RL Peptides 9:681-686(1989)

CC -!- FUNCTION: Hypertrehalosaemic factors are neuropeptides that corpodydrate the level of trehalose in the hemolymph (trehalose is the major carbohydrate in the hemolymph of insects).

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SUBCELLULAR LOCATION: PRO2056; AKH.

DR PROSITE; PS00256; AKH.

DR PROSITE; PS00256; AKH.

KW Neuropeptide; Amidation; Flight, Pyrrolidone carboxylic acid.

KW Neuropeptide; Amidation; Flight, Pyrrolidone Carboxylic acid.

FT MOD RES 10 10 AMIDATION.

SEQUENCE 10 AA; 1163 MW; 056236745771A9C4 CRC64;
 MEDLINE=92321768; PubMed=1622206;
Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,
 "Purification and characterization of a new bacteriocin isolated from
 Gaps
 ..
0
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha; Acridoidea; Romaleidae; Romalea.
 Query Match
29.5%; Score 18; DB 1; Length 10;
Best Local Similarity 33.3%; Pred. No. 1.2e+03;
Matches 3; Conservative 2; Mismatches 4; Indels
 Carnobacterium sp. (strain U149).
Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;
 Query Match 29.5%; Score 18; DB 1; Length 7; Best Local Similarity 100.0%; Pred. No. 1.4e+05; Matches 4; Conservative 0; Mismatches 0; Indels
 7 AA; 786 MW; 741776D05B05B810 CRC64;
 NOV-1990 (Rel. 16, Created)
01-FBB-1994 (Rel. 28, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Romalea microptera (Lubber grasshopper)
 01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Lantibiotic carnocin U149 (Fragment).
 7 AA.
 (Rel. 29, Created)
(Rel. 29, Last seq
(Rel. 40, Last ann
 STANDARD;
 NCBI_TaxID=35782;
 3 SEIO 6
 2 SEIO 5
 Carnobacterium
 01-JUN-1994
01-JUN-1994
 HTF1 ROMMI
P18110;
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SEQUENCE
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SEQUENCE.
RESULT 2
LANC_CARUI
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 -i- FUNCTION: Mediates visceral muscle contractile activity (myotropic
 Gaps
 Duve H., Johnsen A.H., Meestro J.-L., Scott A.G., Winstanley D., Davey M., East P.D., Thorpe A.;
"Lepidopteran peptides of the allatostatin superfamily.";
Peptides 18:1301-1309(1997).
-!- SIMILARITY: Belongs to the allatostatin family.
Neuropeptide, Amidation.
 ..
 Bukaryota; Metazoa; Artiropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
Acridoidea; Acrididae; Oedipodinae; Locusta.
NCBI_TaxID=7004;
 Cydia pomonella (Codling moth).
Bukaryota, Metazoa, Arthropoda; Hexapoda, Insecta; Prerygota,
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Tortricoidea, Tortricidae; Olethreutinae; Cydia.
 TISSUB=COrpora cardiaca;
MEDLINE=90341077; PubMed=1974346;
Schoofs L., Holman G.M., Hayes T.K., Tips A., Nachman R.J., Vandesande F., de Loof A.;
"Isolation, identification and synthesis of locustamyotropin (Lom-MT), a novel biologically active insect peptide.";
Peptides 11:427-433(1990).
 Length 12;
 MOD RES 12 12 AMIDATION.
SEQUENCE 12 AA; 1213 MW; D766C92722D6DDDD CRC64;
 0B2879C45B573767 CRC64;
 -1- SIMILARITY: Belongs to the pyrokinin family. PIR, A43975, A43975. Interpro, IPR001484; Pyrokinin. PROSITE; PS00539; PYROKININ; 1
 Score 17; DB 1; I
Pred. No. 2.3e+03;
 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
 01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-AUG-1991 (Rel. 19, Last annotation update)
Locustamyotropin 1 (LOW-MT-1).
Locusta migratoria (Migratory locust).
 8 AA.
 12 AA
 0; Mismatches
 Neuropeptide, Amidation, Pyrokinin.
MOD_RES 12 AMIDAT
 PRT;
 TISSUE=Larva;
MEDLINE=98054539; PubMed=9392829;
 Cydia pomonella (Codling moth)
 27.9%;
45.5%;
 8 AA; 936 MW;
 5; Conservative
 STANDARD;
 STANDARD;
 1 AVSEIQFMHNL 11
 2 AVPAAOFSPRL 12
 Best Local Similarity
Matches 5; Conserv
 NCBI_TaxID=82600;
 Cydiastatin 6.
 activity)
RESULT 4
LMT1 LOCMI
ID LMT1 LOCMI
AC P22395;
 ALL6_CYDPO
P82157;
 SEQUENCE
 SEQUENCE
 SEQUENCE
 Query Match
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Gaps .. us-09-730-174a-6.closed.rsp

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ö
 SPECIES=C.morosus, TISSUE=Corpora cardiaca; MEDLINE=93129188; PubMed=1482345; Gaede G., Kellner X., Rinehart K.L. Jr., Proefke M.L.; Gaede G., Kallner X., Rinehart K.L. Jr., Proefke M.L.; a tryptophan-substituted member of the AKH/RPCH family isolated from a stick insect corpus cardiacum."; Biochem. Biophys. Res. Commun. 189:1303-1309(1992).
 -1- FUNCTION: Hypertread comming factors are neuropeptides that elevate the level of trehalose in the hemolymph (trehalose is the major carbohdrate in the hemolymph of insects).
-1- SUBCELLULAR LOCATION: Secreted.
-1- MASS SPECTROMETRY: NW=1308.61; METHOD=FAB.
-1- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
-1- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
-1- SIMILARITY: Bolongs to the AKH / HRTH / RPCH family.
 SPECIES=E.tiaratum; TISSUB=Corpora cardiaca; MEDLINE=9053559; PubMed=2340112; Gaede G., Rinehart K.L. del. "Primary structures of hypertrehalosaemic neuropeptides isolated from
 Gaps
 the corpora cardiaca of the cockroaches Leucophaea maderae, Gromphadorhina portentosa, Blattella germanica and Blatta orientalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment mass spectrometry.";
Biol. Chem. Hoppe-Seyler 371:345-354(1990).
 01-JUL-1989 (Rel. 11, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypertrehalosaemic factor II (HTF-II) (Hypertrehalosaemic
 PIR, 809138, 809139.
InterPro; IPR002047, AKH.
PR081TE; PS00256; AKH. 1.
Neuropeptide; Amidation; Glycoprotein; Pyrrolidone carboxylic acid.
MOD RES. 1 PYRROLIDONE CARBOXYLIC ACID.
R C-LINKED (MAN) (PROBABLE).
 Extatosoma tiaratum (Stick insect), and
Extatosoma tiaratum (Stick insect).
Eukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Phasmatodea; Euphasmida; Phasmatoidea;
Heteronemiidae; Carausius.
 SPECIES=C.morosus; TISSUE=Corpora cardiaca;
MEDLINE=8115.7103; PubMed=3828078;
Gaede G., Rinehart K.L. Jr.;
"Primary structure of the hypertrehalosaemic factor II from the
corpus cardiacum of the Indian stick insect, Carausius morosus,
determined by fast atom bombardment mass spectrometry.";
Biol. Chem. Hoppe-82yler 368:67-75(1987).
 ..
0
 26.2%; Score 16; DB 1; Length 10; 33.3%; Pred. No. 2.9e+03; ative 2; Mismatches 4; Indels
 26.2%; Score 16; DB 1; Length 8; 40.0%; Pred. No. 1.40+05; ive 2; Mismatches 1; Indels
 AMIDATION.
9B9036745771A9D1 CRC64;
 neuropeptide II).
Carausius morosus (Indian stick insect), and
 10 AA.
 PRT;
 10 10
10 AA; 1164 MW;
 Query Match
Best Local Similarity 33.30,
 CARBOHYDRATE-LINKAGE SITE.
Query Match
Best Local Similarity 40.00
Matches 2; Conservative
 STANDARD;
 8 MHNLG 12
 3 LYNFG 7
 CARMO
 SEQUENCE
 SEQUENCE
 RESULT 6
HTF2_CARMO
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 Gaps
 Gaps
 Wabhitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.; "Peptides from the skin glands of the Australian buzzing tree frog Litori electrica. Comparison with the skin peptides from Litoria
 Litoria rubella (Desert tree frog).

Bukaryota, Metazoa; Chordata, Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
Pelodryadinae; Litoria.
 ..
0
 FUSS FUSSO STANDARD, PRT; 8 AA.
P81010,
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Dast annotation update)
Pusarium solani (subsp. pisi) (Nectria haematococca).
Eukaryota; Fungi; Ascomycoca; Perizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
 ..
 24.6%; Score 15; DB 1; Length 5; llarity 66.7%; Pred. No. 1.4e+05; Conservative 1; Mismatches 0; Indels
 0; Indels
 24.6%; Score 15; DB 1; Length 8; larity 66.7%; Pred. No. 1.40+05; Conservative 1; Mismatches 0; Indels
 Verma J., Gangal S.V.;
Submitted (JUL-1997) to Swiss-Prot.
-!- ALLERGEN: Causes an allergic reaction in human.
 Amphibian defense peptide; Amidation.
MOD RES 5 5 AMIDATION.
SEQUENCE 5 AA; 630 MW; 668761F2C9A00000 CRC64;
 8 8 AA; 898 MW; C372C441F5B69041 CRC64;
 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Electrin 3
 5 AA.
 Secreted.
 SEQUENCE.
STRAIN=IARI 3596; TISSUE=Mycelium;
 TISSUE=Skin secretion;
 Query Match
Best Local Similarity
1 OLTFIPNWG
 Query Match
Best Local Similarity
 9 HNL 11
 FMH 9
 5
 Allergen.
NON TER
SEQUENCE
 7
 SEQUENCE
 FUSS_FUSSO
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RESULT 9 EFG\_CLOPA

Gaps

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4 EIQFMHNLG 12

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MEDLINE=98054539; PubMed=9392829
 NON TER 11 11
SEQUENCE 11 AA; 1099 MW;
 4 AA; 549 MW;
 Query Match
Best Local Similarity 50.0.
 2; Conservative
 STANDARD;
 STANDARD;
 Neuropeptide; Amidation.
HSC-2DPAGE; P49820; DOG.
 Best Local Similarity
 PIR; A35779; A357
 7 FMHN 10
 NCBI_TaxID=6110;
 1 FLRN 4
 7 FMH 9
 7 FVH 9
 Antho-RNamide.
 IISSUE=Larva;
 CYDPO
 FLRN ANTEL
P58707;
 MOD_RES
SEQUENCE
 SEQUENCE
 Query Match
 P82158;
 group."
 RESULT 12
ALL7_CYDPO
 FLRN ANTEL
 ALL7
 Matches
 RESULT 11
 SOFTWAR
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 "Two-dimensional gel electrophoresis separation and N-terminal sequence analysis of proteins from Clostridium pasteurianum W5."; Electrophoresis 19:802-806 (1998).
-!- FUNCTION: This protein promotes the GTP-dependent translocation of the nascent protein chain from the A-site to the P-site of the
 dog heart proteins.";
Electrophoresis 18:279-5-2802(1997).
Electrophoresis 18:279-5-2802(1997).
CHAIN. TRANSFER OF ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
TO BE UBICULNONE. COMPONENT OF THE FLAVOPROTEIN-SULFUR (FP)
TRAGMENT OF THE ENZYME.
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
-!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
-!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
-!- SUBUNIT: Mammalian complex I is composed of 45 different subunits.
-!- SUBUNIT: Mammalian complex I is composed of 45 different subunits.
-!- SUBUNIT: Belongs to the complex I 24 kDa subunit family.
 Gaps
 -:- SUBCELLULAR LOCATION: Cytoplasmic.
-:- SIMILARITY: Belongs to the GTP-binding elongation factor family.
EF-G/EF-2 subfamily.
InterPro: IPR00775; EF GTPbind.
PROSITE: PS00301; EFACTOR GTP; PARTIAL.
BLONGARION factor; Protein blosynthesis; GTP-binding.
NON_TER.
 Dunn M.J., Corbett J.M., Wheeler C.H., "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
 Canis familiaris (Dog)
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
VCBI_TaxID=9615;
 Clostridium pasteurianum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
 ö
 01-OCT-1996 (Rel. 34, Created)
Lb-UTL-1998 (Rel. 36, Last sequence update)
10-CCT-2003 (Rel. 42, Last amocation update)
NADH-ubiquinone oxidoreductase 24 kDa subunit (EC 1.6.5.3)
 24.6%; Score 15; DB 1; Length 11; 25.0%; Pred. No. 5.18+03; ive 3; Mismatches 3; Indels
 SEQUENCE 11 AA; 1337 MW; 412E71F1D9C33B17 CRC64;
 annotation update) (CP 5) (Fragment).
 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update
Elongation factor G (EF-G) (CP 5) (FF-C-C)
FUSA.
 11 AA
 11 AA
 PRT;
 STRAIN=W5;
MEDLINE=98291870; PubMed=9629918;
Flengsrud R., Skjeldal L.;
 TISSUE=Heart;
MEDLINE=98163340; PubMed=9504812;
 2; Conservative
 1.6.99.3) (Fragment)
 STANDARD;
 STANDARD;
 5 IQFMHNLG 12
 4 LEKFONIG 11
 Best Local Similarity
 NCBI_TaxID=1501;
 NUHM CANFA
P49820;
 EFG CLOPA
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 Query Match
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 MEDLINE=90319122; PubMed=1973541; Grimmelikhuijzen C.J.P., Rinnehart K.L. Jr., Jacob E., Graff D., Reinneneid R.K., Nothacker H.-P., Staley A.L.; Antho-Rwamide), a sea anemone neuropeptide containing an unusual amino-terminal blocking
 Gaps
 Gaps
 Anthopleura elegantissima (Sea anemone).
Eukaryota, Metazoa, Cnidaria, Anthozoa, Zoantharia, Actiniaria,
Nynantheae, Actiniidae, Anthopleura.
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InterProj | PR002023; Cmplx1 24kDa.
PROSITE; PS01099; COMPLEX1 24kDa.
PROSITE; PS01099; COMPLEX1 24k; PARTIAL.
Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Metal-binding;
Iron-sulfur; Iron; 2Fe-2S.
NON_TER 11 11 11
 Cydia pomonella (Codling moth).

Eukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;

Eukaryota, Budopterrygota; Lepidoptera; Glossata; Ditrysia;

Tortricoidea; Tortricidae; Olethreutinae; Cydia.

NCBI_TaxID=82600;
 Length 11;
 Score 14; DB 1; Length 4;
Pred. No. 1.4e+05;
1; Mismatches 1; Indels
 267F5369C9C72DD8 CRC64;
 AMIDATION.
64540729A0000000 CRC64;
 Score 15; DB 1; Ler
Pred, No. 5.1e+03;
 Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414(1990)
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Neuron specific.
-!- MASS SPECIFOMETRY: WW=549.3; METHOD=FAB.
 L-3-PHENYLLACTYL.
 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
 7 AA.
 4 AA.
 1; Mismatches
 PRT;
 SEQUENCE, AND MASS SPECTROMETRY
 24.6%;
 23.0%;
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Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 TISSUE-Cerebral ganglion, and Thoracic ganglion; MEDLINE-98121193; PubMed-9461295;
 Cydiastatin 1.
 SEQUENCE
 SEQUENCE
 Query Match
 RESULT 15
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 Tryptophyllin 5.1.
Litoria rubella (Desert tree frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Amphibia, Batrachia, Anura, Neobatrachia, Hyloidea, Hylidae;
Pelodryadinae, Litoria.
 .
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 .
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley Davey M., East P.D., Thorpe A.; "Lepidopteran peptides of the allatostatin superfamily."; Peptides 18:1301-1309(1997).
 Carcinus maenas (Common shore crab) (Green crab).
Eukaryota, Metazoa, Arthropoda, Crustacea, Malacostraca,
Eumalacostraca, Eucarida, Decapoda, Pleocyemata, Brachyura,
Eubrachyura, Portunoidea, Portunidae, Carcinus.

NCBI_TaxID=6759,
 23.0%; Score 14; DB 1; Length 7; 40.0%; Pred. No. 1.4e+05; ive 2; Mismatches 1; Indels
 PYRROLIDONE CARBOXYLIC ACID. AMIDATION.
 Length 7;
 2; Indels
 -!- SIMILARITY: Belongs to the allatostatin family.
Neuropeptide; Amidation.

AMIDATION.
 7 7 AA; 873 MW; 672879CABB569350 CRC64;
 7 AA; 983 MW; 7401E9D3676046B0 CRC64;
 23.0%; Score 14; DB 1; I
33.3%; Pred. No. 1.4e+05;
ive 2; Mismatches 2;
 30-VAY-2000 (Rel. 39, Created)
30-WAY-2000 (Rel. 39, Last sequence update)
30-WAY-2000 (Rel. 39, Last annotation update)
 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
 7 AA.
 8 AA.
 SEQUENCE, AND MASS SPECTROMETRY.
 Best Local Similarity 40.C
Matches 2; Conservative
 STANDARD;
 2; Conservative
 STANDARD;
 Query Match
Best Local Similarity
 8 MHNLG 12
 NCBI_TaxID=104895;
 4 EIQFMH 9
 |::|
2 MYDFG 6
 Carcinustatin 18
 : | : |
1 QIPWFH
 LITRU
 AL18 CARMA
P81821;
 MOD_RES
SEQUENCE
 SEQUENCE
 Query Match
 TYS1 LIT
P82065;
 RESULT 13
TYS 1_LITRU
TYS 1_LITRU
DT 28-FEBB
DT 28-FEBB
DT 10-CFB
DE TYPPIO
OC EUKATY,
OC PEIDE
OC NCBI OT
OC
 RESULT 14
ALIB CARNA
ALIB CARNA
DO 30-MAY
DT 30-MAY
DT 30-MAY
DT 30-MAY
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CO CARNA
CO EUMAIA
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 Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D., Davey M., East P.D., Thorpe A.,
"Lepidopteran peptides of the allatostatin superfamily.";
Peptides 18:1301-1309(1997).
-- SIMILARITY: Belongs to the allatostatin family.
Nouropeptide; Amidation.
MOD_RES MIDATION.
"Insignation and identification of multiple neuropeptides of the allatostatin superfamily in the shore crab Carcinus maenas.";
Eur. J. Biochem. 250:7274(1997).
-!- FUNCTION: May act as a neurotransmitter or neuromodulator.
-!- SIMILARITY: Belongs to the allatostatin family.
Nouropeptide, Amidation, Multigene family.
MOD RES

SEQUENCE 8 AA, 919 MW; C82879D5AB569AB5 CRC64;
 ·,
 .,
 23.0%; Score 14; DB 1; Length 8; 40.0%; Pred. No. 1.4e+05; ative 2; Mismatches 1; Indels
 1; Indels
 Cydia pomonelia (Codling moth).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pteryo
Neoptera, Endopteryota, Lepidoptera, Glossata, Dirrysia
Tortricoidea, Tortricidae, Olethreutinae, Cydia.
 i, Indels
 23.0%; Score 14; DB 1; Length 8; llarity 50.0%; Pred. No. 1.40+05; Conservative 1; Mismatches 1; Indels
 8 8 AMIDATION.
8 AA; 934 MW; C82879C45B51F775 CRC64;
 ALL1_CYDPO STANDARD; PRT; 8 AA. P82152; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update)
 Search completed: September 5, 2004, 09:35:03
 MEDLINE=98054539; PubMed=9392829;
 Ouery Match
Best Local Similarity 40.v
 Local Similarity
les 2; Conserv
 8 MHNLG 12
 3 MYSFG 7
 9 HNLG 12
 NCBI TaxID=82600
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Q9PS71
 RESULT 1
Q9PS71
 September 5, 2004, 09:30:03; Search time 27.5 Seconds (without alignments) 137.681 Million cell updates/sec
 2565
GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 1017041 segs, 315518202 residues
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 SPTRENBL 25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_lnugi:*
4: sp_lnuman:*
5: sp_lnuman:*
5: sp_mammal:*
7: sp_mhc:*
7: sp_plage:*
7: sp_plage:*
7: sp_plage:*
7: sp_volent:*
7: sp_volent
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 1 AVSEIQFMHNLG 12
 US-09-730-174A-6
61
 Minimum DB seq length: 0 Maximum DB seq length: 12
 Scoring table:
 Perfect score:
 Database :
 Sequence:
 Searched:
 Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

|           |        | Description | Q9ps71 aqkistrodon | 09tt78 canis famil | 092766 canine dist | 071066 canine dist | P82081 limnodynast | 013591 saccharomyc | O8mes0 anoda crist | 085631 avian carci | 023876 dictvosteli | P82085 limnodynast | Q28742 oryctolagus | 005403 saccharomyc | 040659 orvza sativ | P82082 limnodynast |        | Q44377 aeromonas t |
|-----------|--------|-------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|
| SUMMARIES |        | σī          | Q9PS71             | Q9TT78             | 092766             | 071066             | P82081             | 013591             | QBMESO             |                    | 023876             | P82085             | Q28742             | Q05403             | Q40659             | P82082             | P82083 | Q44377             |
|           |        | DB          | 13                 | 9                  | 12                 | 12                 | 13                 | m                  | φ                  | 15                 | ហ                  | 13                 | w                  | ٣                  | 10                 | 13                 | 13     | 7                  |
|           | Query  | Length      | 11                 | œ                  | σ                  | 6                  | 12                 | 80                 | 12                 | 12                 | 11                 | 12                 | 7                  | ω                  | α                  | α                  | 80     | σv                 |
| ď         | Query  | Match       | 39.3               | 31.1               | 31.1               | 31.1               | 31.1               | 29.5               | 29.2               | 29.5               | 27.9               | 27.9               | 26.2               | 26.2               | 26.2               | 26.2               | 26.2   | 26.2               |
|           |        | Score       | 24                 | 19                 | 19                 | 19                 | 19                 | 18                 | 18                 | 18                 | 17                 | 17                 | 16                 | 16                 | 16                 | 16                 | 16     | 16                 |
|           | Result | No.         | н                  | 7                  | ო.                 | ΄4                 | ស                  | 9                  | 7                  | ω                  | თ                  | 10                 | 11                 | 12                 | 13                 | 14                 | 15     | 16                 |

| Q44468 aeromonas v<br>O8rku3 borrelia bu | 8 aeromonas |        | lilium lo | spinacia | spina  |        | mnsid  | Jomo S | Q34909 locusta miq |        |        | Q15891 homo sapien |        |        | Q15342 homo sapien | omby   |        | Q9c057 homo sapien | obuo   | Q9bdq9 gorilla gor | 0      | pan    | hom    | 2 gnath | 9534   | 084156 orf virus ( | 960 | r |            |
|------------------------------------------|-------------|--------|-----------|----------|--------|--------|--------|--------|--------------------|--------|--------|--------------------|--------|--------|--------------------|--------|--------|--------------------|--------|--------------------|--------|--------|--------|---------|--------|--------------------|-----|---|------------|
| Q44468<br>O8RKII3                        | 043928      | 044001 | Q9FXL0    | P82132   | P82133 | Q9GD68 | P82336 | Q15894 | Q34909             | 090493 | Q43960 | Q15891             | Q8S3C6 | Q9FEC0 | Q15342             | P82222 | Q8GZC8 | Q9C057             | Q9BDC8 | Q9BDQ9             | Q9BDD0 | Q9BDC9 | Q9UMV5 | 099182  | Q49534 | 10                 | 0   |   | ALIGNMENTS |
| OI O                                     |             |        |           |          |        |        |        |        |                    |        |        |                    |        |        |                    |        |        |                    | 9      | 9                  | 9      | ø      | 4      | ω       | C)     | 12                 | 13  |   |            |
| თ თ                                      | 0           | 9      | σ         | 10       | 10     | 11     | ij     | œ      | œ                  | œ      | σ      | σ                  | Q      | on     | 10                 | 10     | 10     | 11                 | 17     | 11                 | 11     | 11     | 12     | 7       | œ      | œ                  | 80  |   |            |
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| 17                                       | 13          | 20     | 21        | 22       | 23     | 24     | 25     | 26     | 27                 | 28     | 53     | 30                 | 31     | 32     | 33                 | 34     | 35     | 36                 | 37     | 38                 | 39     | 40     | 41     |         | 43     |                    | 45  |   |            |

#### TREMEDIA

AC GPBS71 PRELIMINARY; PRT; 11 AA.

C GPBS71, DT Created)

DT 01-YAY-2000 (TrEMBLrel. 13, Last sequence update)

DE Starsyota metalloproceinase (Fragment).

C Editorosuria, Squamata, Scleroglossa, Serpentes, Colubroidea,

C Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,

C Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,

C Viperidae, Crotalinae, Agkistrodon.

RN 101

RN SEQUENCE

RA MEDINNE-31378546; PubMed=1898066;

RA Guam A.L., Retzios A.D., Henderson G.N., Markland F.S.Jr.;

RY 6 the southern copperhead snake (Agkistrodon contortrix

RT 6 the southern copperhead snake (Agkistrodon contortrix

RT 7 Arch. Blochem: Biophys. 289:197-207(1991).

RT Arch. Blochem: Biophys. 289:197-207(1991).

SEQÜENCE 11 AA; 1209 MW; 7CAO2DID41B8772B CRC64;

SEQÜENCE 11 AA; 1209 MW; 7CAO2DID41B8772B CRC64;

Autches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

A HILG 12

DD 7.HNLG 10

RESULT 2 OSTITA PRELIMINARY: PRI ID OSTITA PRELIMINARY: PRIT

O9TT78 PRELIMINARY, PRT; 8 AA.

AC Q9TT78 PRELIMINARY,

DT 01-MAY-2000 (TEMBLE-1 13, Created)

DT 01-MAY-2000 (TEMBLE-1 13, Last sequence update)

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ö SEQUENCE FROM N.A.

STRAIN=DOG #5556/89;
Liermann H., Harder T., Haas L.;
Liermann H., Harder T., Haas L.;
Genetic analysis of the central untranslated genome region and the
proximal coding part of the F gene of wild-type and vaccine distemper
morbilliviruses.";
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.

BMBL; AF026237; AAC09167.1;
NON\_TER Gaps . 0 Query Match
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 0; Indels Viruses; ssRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Paramyxovirinae; Morbillivirus. NCBI\_TaxID=11232; Last sequence update) Last annotation update) SEQUENCE 9 AA; 1011 MW; F281732760533441 CRC64; 9 AA. Created) 8 MHN 10 MHN 3 RESULT 4 071066 à d

Canine distemper virus. Viruses; ssRNA negative-strand viruses; Mononegavirales;

Last sequence update) Last annotation update)

01-AUG-1998 (TrEMBLrel. 07, 01-AUG-1998 (TrEMBLrel. 07, 01-DEC-2001 (TrEMBLrel. 19, Fusion protein (Fragment).

OC CENTRAL DESCRIPTION OCCORDATE DESCRIPTION OCCORDATE DESCRIPTION OCCURRENCE DESCRIPTION O

Created)

9 AA.

PRELIMINARY;

071066

Liermann H., Harder T., Haas D.;
"Genetic analysis of the central untranslated genome region and the proximal coding part of the F gene of wild-type and vaccine distemper morbilliviruses.";
EMBL: AF026234; AAC09164.1; -. Limnodynastes terraereginae (Northen banjo frog). Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Amphibia, Batrachia, Anura, Neobatrachia, Bufonoidea, Myobatrachidae, Limnodynastinae, Limnodynastes. TISSUBLACE, AND MASS SPECTROMETRY.

TISSUB-TIBIAL GLAND;

Raftery M.J., Bradford A.M., Bowie J.H., Wallace J.C., Tyler M.J.;

Raftery M.J., Bradford A.M., Bowie J.H., Wallace J.C., Tyler M.J.;

Peptides from Australian frogs. The structure of the dynastins from the banjo frogs Limmodynastes interioras, Limmodynastes dumerilii and Limmodynastes terraereginae.";

Aust. J. Chem. 46:833-842(1993)

Aust. J. Chem. 46:833-842(1993)

SEQUENCE 12 AA; 1236 MW; 147AA70EDF472724 CRC64; Gaps Gaps Saccharomyces cerevisiae (Baker's yeast). Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces. ·. . 0 31.1%; Score 19; DB 13; Length 12; 60.0%; Pred. No. 7.1e+03; 31.1%; Score 19; DB 12; Length 9; 100.0%; Pred. No. 1e+06; ative 0; Mismatches 0; Indels Indels Obermaier B., Piravandi B., Rinke M.; Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases. [2] 013591, 01-JAN-1998 (TrEMBLrel. 05, Created) 01-JNOV-1999 (TrEMBLrel. 12, Last sequence update) 01-0CT-2002 (TrEMBLrel. 22, Last annotation update) 0RF YNL337W (Fragment). 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAY-2000 (TrEMBLrel. 13, Last annotation update) SEQUENCE 9 AA; 1124 MW; F29D045760440441 CRC64; Paramyxoviridae; Paramyxovirinae; Morbillivirus. NCBI\_TaxID=11232; 12 AA. 2; Mismatches PRT; Local Similarity 100. nes 3; Conservative 3; Conservative PRELIMINARY; PRELIMINARY; SEQUENCE FROM N.A. STRAIN=Dog #10757/96; Best Local Similarity 8 MHNLG 12 NCBI\_TaxID=4932; 8 MHN 10 1 MHN 3 Query Match Best Local & Query Match P82081 P82081; 013591 Matches RESULT 6 013591 Matches RESULT 5 P82081 SORRERERES ò SOCCE SERVICE SOCCE SOCC ਨੇ g

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72E4B884F30736DB CRC64;

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12 AA; 1466 MW;
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 9 HNL 11
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 Gaps
 Chloroplast.

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II; Malvales, Malvaceae, Malvoideae; Anoda.
 SEQUENCE FROM N.A.

Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;

Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using chloroplast DNA sequences of ndhF and the rpl16 intron.";

Syst. Bot. 27:33-350 (2002).

EMBL; AF384567; AAM50405.1;

GO; GO:0009507; C:chloroplast; IEA.
 SEQUENCE FROM N.A.
MEDINE=85033920; PubMed=6092695;
Sutrave P., Jansen H.W., Bister K., Rapp U.R.;
Sutrave P., Jansen H.W., Bister K., Rapp U.R.;
"3'-terminal region of avian carcinoma virus MH2 shares sequence elements with avian sarcoma viruses Y73 and SR-A.";
J. Virol. 52:703-705(1984).
NON_TER NOTER
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 Query Match
29.5%; Score 18; DB 8; Length 12;
Best Local Similarity 37.5%; Pred. No. 1.1e+04;
Matches 3; Conservative 3; Mismatches 2; Indels
 Query Match
29.5%; Score 18; DB 3; Length 8;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 1; Indels
 Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MH2, proviral DNA, myc to 3' LTR (Fragment).
Avian carcinoma virus.
Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
 NON TER 1 1
NON TER 12 12
SEQUENCE 12 AA; 1431 MW; 9A5E59B65452C9CA CRC64;
 01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Ribosomal protein 16 (Fragment).
 8 AA; 1005 MW; 5CA441E449C9C720 CRC64;
 PRT;
 PRELIMINARY;
 PRELIMINARY;
 | |::|:
3 EPDFVNNI 10
 4 EIQFMHNL 11
SEQUENCE FROM N.A.
 7 FMHN 10
 4 FNHN 7
 Anoda cristata.
 Chloroplast
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 Q85631
Q85631;
 Q8MES0
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 Limnodynastes salmini (Salmin's-striped frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
Limnodynastinae; Limnodynastes.
NCBI_TaxID=39404;
 SEQUENCE, AND MASS SPECTROMETRY.
TISSUB-SKIN SECRETION;
Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;
"Peptides from Australian frogs. The structure of the dynastins from Limnodynastes salmini and Fletcherin from Limnodynastes fletcheri.";
Aust. J. Chem. 46:135-1244(1993).
-!- MASS SPECTROMETRY: NM-1114; METHOD-FAB.
SEQUENCE 12 AA, 1114 MW; 3AB5A976CAA72728 CRC64;
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(3
 Length 12;
 Score 17; DB 13; Length 12;
Pred. No. 1.8e+04;
2; Mismatches 2; Indels
 Query Match 27.9%; Score 17; DB 5; Length 11; Best Local Similarity 28.6%; Pred. No. 1.6e+04; Matches 2; Conservative 4; Mismatches 1; Indels
 MEDLINE=8226045; PubMed=6286214; MEDLINE=8226045; PubMed=6286214; MCKeon M.; Firtel R.A.; MCKeon M.; Firtel R.A.; Cold Spring Harb. Symp. Quant. Biol. 46:495-505(1982). Cold Spring Harb. Symp. Quant. Biol. 46:495-505 (1982). EMBL; K02956; AAA33150.1; JOINED. SEQUENCE 11 AA, 1205 MW; 728B4C14C6C2CAAB CRC64;
 Dictyostelium discoideum (Slime mold).
Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
NCBL_TaxID=44689;
 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DYNASTIN 7.
29.5%; Score 18; DB 15; L 100.0%; Pred. No. 1.1e+04; tive. 0; Mismatches 0;
 11 AA.
 12 AA.
 27.9%;
 6, Conservative
 PRELIMINARY;
 PRELIMINARY;
 1 AVSEIOFMHNLG 12
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AVSGL--LTNLG 11
 4 EIQFMHN 10
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Limnodynastes salmini (Salmin's-striped frog).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Alpha-amylase (Fragment).
Oryas sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
 MEDLINE=91078641; PubMed=2258052;
Kungai M.H., Shah M., Terashima M., Vrkljan Z., Whitaker J.R.,
Rodriquez R.L.,
"Expression and secretion of rice alpha-amylase by saccharomycers
 Score 16; DB 10; Length 8; Pred. No. 1e+06;
 8 AA.
 4; Mismatches
 PRT;
 Limnodynastinae, Limnodynastes.
NCBI_TaxID=39404;
 cerevisiae ";
Gene 94:209-216(1990).
EMBL; M62916; AAA33892.1; -.
Gramene; Q40659; -.
 h 26.2%;
Similarity 28.6%;
2; Conservative '
 3; Conservative
 PRELIMINARY;
 5 IQFMHNL 11
 Best Local Similarity
Matches 3; Conserv
 Query Match
Best Local Similarity
Matches 2; Conserv
 1 MOVLNNM 7
 SEQUENCE FROM N.A.
 NCBI_TaxID=4530;
 10 NLG 12
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 DYNASTIN 5.
 DYNASTIN 4.
 Query Match
 P82082
 RESULT 15
P82083
AC P8208
AC P8208
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 "Characterization of genomic clones specifying rabbit alpha- and beta-
 Zumstein E., Pearson B.M., Kalogeropoulos A., Schweizer M.;
"A 29,425 kb segment on the left arm of yeast chromosome XV contains more than twice as many unknown as known open reading frames."; Yeast 11:975-986(1995).

EMBL, X83121; CA58183.1; -.
 Gaps
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 Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
 Eukaryota; Fungi, Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetales;
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 MEDLINE-84221901; PubMed-6328491;
Friedman D.J., Umeda P.K., Sinha A.M., Hsu H.-J., Jokovcic S.,
Rabinowitz M.;
 26.2%; Score 16; DB 6; Length 7; 60.0%; Pred. No. 1e+06; ative 1; Mismatches 1; Indels
 26.2%; Score 16; DB 3; Length 8; 50.0%; Pred. No. 1e+06; arive 2; Mismatches 0; Indels
 005403;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DNA for ORF'S from chromosome XV (Fragment).
 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 8 AA; 879 MW; 7B5322D2C441E058 CRC64;
 7 AA; 916 MW; 6B1B1AA1E69326B0 CRC64;
 Created)
Last sequence update)
 ventricular myosin heavy chains.";
Proc. Natl. Acad. Sci. U.S.A. 81:3044-3048(1984).
EMBL; K01698; AAA31415.1;
PIR; 146868; 146868.
NON_TER
 8 AA.
 7 AA.
 Saccharomyces cerevisiae (Baker's yeast)
 Alpha-myosin heavy chain (Fragment)
 PRT;
 STRAIN=FY1679;
MEDLINE=96021609; Pubmed=8533473;
 Q40659;
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
 Query Match
Best Local Similarity 50..
2, Conservative
 3; Conservative
 PRELIMINARY;
 PRELIMINARY;
 PRELIMINARY;
 Query Match
Best Local Similarity
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 6 QFMHN 10
 | ||:
1 QKMHD 5
 8 MHNL 11
 NCBI_TaxID=9986;
 NCBI_TaxID=4932;
 IHNV 5
 SEQUENCE
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SEQUENCE
 Q28742
Q28742
 040659
 005403
 RESULT 13
Q40659
ID Q4065
AC Q4065
DT 01-NO
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 RESULT 12
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 Matches
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 Limnodynastes salmini (Salmin's-striped frog).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;

Limnodynastinae; Limnodynastes.
 Gaps
 .
26.2%; Score 16; DB 13; Length 8; 100.0%; Pred. No. 1e+06; tive 0; Mismatches 0; Indels
 P82083 PRELIMINARY; PRT; 8 AA. P82083.
P0.1-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
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OX NCBL_TaxID=39404;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE-SKIN SECRETION;
RA Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "Peptides from Australian frogs. The structure of the dynastins from Limnodynastes salamin and Pletcherin from Limnodynastes fletcheri.";
RL Aust. J. Chem. 46:1235-1244(1993).
CC -1- MASS SPECTROMETRY: MM=786; METHOD=FAB.
SQ SEQUENCE 8 AA; 786 MW; 7858772455B05728 CRC64;
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Query Match 26.2%; Score 16; DB 13; Length 8; Best Local Similarity 100.0%; Pred. No. 1e+06; Matches 3; Conservative 0; Mismatches 0; Indels

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5, 2004, 09:26:47; Search time 36.5 Seconds (without alignments) 92.892 Million cell updates/sec
 368311
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 1586107 segs, 282547505 residues
 - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 1 AVSEIQFMHNLG 12
 US-09-730-174A-6
61
 September
 Minimum DB seq length: 0 Maximum DB seq length: 12
 Title:
Perfect score:
 Scoring table:
 OM protein
 Sequence:
 Searched:
 Run on:
```

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries A\_Geneseq\_29Jan04:\* .: geneseqp1980s:\* ?: geneseqp1990s:\* Database :

geneseqp2000s:\*
geneseqp2001s:\*
geneseqp2002s:\*
geneseqp2003as:\*
geneseqp2003bs:\* geneseqp2004s:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Abg72608 Parathyro Aavy5668 Parathyro Aavy5668 Parathyro Aavy68767 Amino aci Abb68219 Human par Abr4166 Human par Abr4166 Human par Aay56600 Resin bou Aab86222 PHN(1-14) Aay56966 Parathyro Aary5696 Parathyro Aary6691 Parathyro Aab86220 Human par Aab66932 Rat parathyro Aab86932 Rat parathyro Aab86931 Rat parathyro Aab86931 Rat parathyro Aab86915 Parathyro Aab86916 Parathyro Aab86916 Parathyro Aab86917 Parathyro Aab96914 Parathyro Aab84769 Parathyro Aaw45785 Parathyro Abp71484 Parathyro Aab82547 (Asnio, T Aab96892 Rat parat Abg72607 Parathyro Description SUMMARIES ABG72607 AAY96968 AAY96968 AAK91644 AAY68767 AAK4166 AAX50600 AAB01862 AAY96966 AAR91645 AAB01863 AAY96981 AAB86220 AAB96932 AAB96931 AAB96915 AAB96915 AAB96915 Query Match Length DB Result No. 

| Abp71485 Parathyro |            | Aab96891 Rat parat | Para       | Aab01864 PTH(1-14) |            |            | Aar91646 Human par | Antiq    | Aab86221 Human par | Comple     | Abu54029 Human DNA |            | -          |          | ω        | Aab01866 PTH(1-14) | 4        | 10 HLA   |          |
|--------------------|------------|--------------------|------------|--------------------|------------|------------|--------------------|----------|--------------------|------------|--------------------|------------|------------|----------|----------|--------------------|----------|----------|----------|
| 5 ABP71485         | 5 ABP71483 | 4 AAB96891         | 3 ABP71482 | 1 AAB01864         | 1 AAY78849 | 1 AAY97062 | : AAR91646         | AAB07467 | AAB86221           | . AAG63991 | ABU54029           | : AAR90421 | : AAY55148 | AAY86894 | AAB00068 | . AAB01866         | ABP83654 | ABP89380 | ABP88771 |
| 11 6               | 11 6       | -                  | _          |                    |            |            | 8                  |          |                    | 0          |                    | 12 2       |            | c)       |          |                    | _        | -        | _        |
| 50.8               | 50.8       | 50.8               | 50.8       | 47.5               | 47.5       | 47.5       | 45.9               | 45.9     | 45.9               | 44.3       | 44.3               | 44.3       | 44.3       | 44.3     | 42.6     | 42.6               | 41.0     | 41.0     | 41.0     |
| 31                 | 31         | 31                 | 31         | 5                  | 29         | 53         | 28                 | 28       | 28                 | 27         | 27                 | 27         | 27         | 27       | 56       | 56                 | 25       | 25       | 25       |
| 26                 | 27         | 28                 | 59         | 30                 | 31         | 32         | 33                 | 34       | 35                 |            |                    | 38         |            | 40       | 41       | 42                 | 43       | 44       | 45       |

### ALIGNMENTS

New parathyroid hormone (PTH) antigenic peptide inducing the formation and isolation of antibodies having an affinity to it, useful for determining bioactive PTH levels in serum, plasma and/or cell culture media. Human, parathyroid hormone, antigen; hypercalcaemia; osteoporosis; primary hyperparathyroidism; mouse; rat; bovine; porcine; canine. Parathyroid hormone antigenic peptide 2-12. Location/Qualifiers ABG72607 standard; peptide; 11 AA. /label= Leu, Phe 05-DEC-2000; 2000US-00730174. 05-DEC-2000; 2000US-00730174 (first entry) Zahradnik RJ, Lavigne JR; (ZAHR/) ZAHRADNIK R J. (LAVI/) LAVIGNE J R. WPI; 2003-066685/06. Mus sp.
Rattus sp.
Bos taurus.
Sus scrofa.
Canis familiaris. Key Misc-difference 6 US2002110871-A1 Homo sapiens 11-FEB-2003 15-AUG-2002 ABG72607; RESULT 1 ABG72607 

The invention relates to a new antigenic peptide for inducing the formation and isolation of antibodies having an affinity to it, being

Claim 1; Page 5; 11pp; English.

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formed from the N-terminus of parathyroid hormone (PTH). Also included are; (1) a method for producing antibodies useful in the determination of PTH levels in a biological sample comprising a transmission of PTH; (b) administering the antigen comprising a peptide fragment of PTH; (b) administering the first peptide antigen to a host animal to induce antibody production; (c) monitoring the antibody titre produced; (d) antibody production; (c) monitoring the antibody titre produced; (d) antibody produced in the host animal; and (e) selecting antisera from the isolated antisera produced in the host that is capable of binding to a second peptide antigen; (2) an antibody (ab) produced by the method; and (3) test kits and analytical procedures used for the determination of bioactive intact PTH utilising (ab). The methods and compositions of the present invention are useful for determining to mit the present invention, as the antigens, antibodies and methods of the present invention, as the antigens, and input the particular advantages of possessing of greater affinity for PTH, and in particular advantages of possessing recognition for antio acid residues extending beyond the first N-terminal PTH residue, and further have negligible cross-reactivity with the large con-molecular forms of PTH. PTH levels are an important parameter in particular advantages of possessing the present interpretate and primary hyperparathyroidism. The present sequence represents and primary forms of particular advantages of possessing the representing amino acids 2-12 of human, mouse, rat, porcine,
 Gaps
 Human, parathyroid hormone; antigen; hypercalcaemia; osteoporosis; primary hyperparathyroidism; mouse; rat; bovine; porcine; canine.
 .;
 Score 50; DB 6; Length 11;
Pred. No. 0.013;
 1; Indels
 0; Mismatches
 Parathyroid hormone antigenic peptide 1-12.
 Location/Qualifiers
 ABG72608 standard; peptide; 12 AA.
 label= Ser, Ala
 82.0%;
90.9%;
 /label= Leu,
 05-DEC-2000; 2000US-00730174
 05-DEC-2000; 2000US-00730174
 Zahradnik RJ, Lavigne JR;
 11-FEB-2003 (first entry)
 Ouery Match
Best Local Similarity 90.9
Marches 10; Conservative
 2 VSEIQFMHNLG 12
 1 VSEIQXMHNLG 11
 (ZAHR/) ZAHRADNIK R J. (LAVI/) LAVIGNE J R.
 Rattus sp.
Bos taurus.
Sus scrofa.
Canis familiaris.
 Key
Misc-difference 1
 Misc-difference 7
 US2002110871-A1
 Sequence 11 AA;
 Homo sapiens.
 15-AUG-2002.
 ABG72608;
 Wus sp
 RESULT 2
 ABG72608
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The invention relates to a new antigenic peptide for inducing the formation and isolation of antiboddes having an affinity to it, being formation and isolation of antiboddes having an affinity to it, being formed from the N-terminus of parathyroid hormone (PFN). Also included are; (1) a method for producing antiboddes useful in the determination of PTN; (b) antibody production; (c) monitoring the post de from the determination of administering the first peptide antigen comprising a peptide fragment of PTN; (b) antibody production; (c) monitoring the antibody titre produced; (d) isolating antisera produced in the host animal, and (e) selecting antisera from the isolated antisera produced in the host that is capable of binding to a second peptide antiser; (2) an antibody (ab) produced by the method; and (3) test kits and analytical procedures used for the determination of bioactive intact PTH utilising (ab). The methods and compositions of the present invention are useful for determining compared to prior art, have the particular advantages of possessing compared to prior art, have the particular advantages of possessing creater affinity for PTH, and in particular, are designed to have a novel crecognition for amino acid residues extending beyond the first N-terminal partners forms of PTH, PTH levels are an important parameter in partners suffering from hyperal camena, osteoporosis and primary contains and the present sequence represents a PTH antigenic contains and better and contains and purmant mouse, rat, porcine, contains and purmant of the present sequence represents a PTH antigenic contains and purmant methods and contains and howing prumants and purmants and pu
 New parathyroid hormone (PTH) antigenic peptide inducing the formation and isolation of antibodies having an affinity to it, useful for determining bioactive PTH levels in serum, plasma and/or cell culture
 Gaps
 PTH; parathyroid hormone; N-terminal; signaling domain; bone mass; bone reformation; resorption; remodeling; tether1; osteoporosis.
 Parathyroid hormone N-terminal signaling domain (residues 1-11).
 0;
 82.0%; Score 50; DB 6; Length 12; 90.9%; Pred. No. 0.014; 1; Indels iive 0; Mismatches 1; Indels
 AAY96968 standard; peptide; 11 AA.
 Claim 2; Page 5; 11pp; English.
 99WO-US031108.
 98US-0114577P.
 (first entry)
 10; Conservative
 2 VSEIQFMHNLG 12
 VSEIQXMHNLG 12
 (GARD/) GARDELLA T J.
(KRON/) KRONENBERG H M.
(POTT/) POTTS J T.
 canine and bovine PTH
 Query Match
Best Local Similarity
 WPI; 2003-066685/06.
 Sequence 12 AA;
 WO200039278-A2.
 Homo sapiens
 0-DEC-1999;
 31-DEC-1998;
 31-OCT-2000
 06-JUL-2000.
 AAY96968;
 Matches
 AAY96968
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Jueppner H;

Potts JT,

us-09-730-174a-6.closed.rag

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Compounds of the structure or formula S-(L) n-B, R 1-S-(L) n-R or S-(L) n-R are new. S is an amino terminal signaling functional domain of parathyroid hormone (PTH); L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R_l is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor sequence. The new compounds are used for treating mammalian conditions reformation, bone resorption and/or bone remodeling, treating diseases and disorders associated with decreased tetherl activity, increasing cAMP in a mammalian cell having PTH-1 receptors, or screening for a peptide or non-peptide PTH (claimed). The new compound can be administered by regular injections to treat osteoporosis
 New antigenic peptide(s) from human parathyroid hormone - and antibodies generated using them, able to distinguish between active and inactive forms of the hormone.
 New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass.
 Human parathyroid hormone antigenic peptide hPTH 1-10.
 AAR91644 standard; peptide; 10 AA
 Claim 4; Page 92; 119pp; English.
 Gardella TJ, Kronenberg HM,
 94DE-04434551
 94DE-04434551
 Claim 2; Page 4; 5pp; German
 Human parathyroid hormone; h diagnosis; active hPTH 1-37.
 (first entry)
 10; Conservative
 1 AVSEIQLMHNL 11
 1 AVSEIQFMHNL 11
 Forssmann
 WPI; 1996-180391/19.
 WPI; 2000-452384/39
 (FORS/) FORSSMANN W.
 Query Match
Best Local Similarity
Matches 10; Conserv
(JUEP/) JUEPPNER
 Sequence 11 AA;
 28-SEP-1994;
 28-SEP-1994;
 DE4434551-A1
 06-NOV-1996
 Adermann K,
 04-APR-1996
 Synthetic
 AAR91644;
 AAR91644
 RESULT
 ठ
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Score 49; DB 3; Length 11; Pred. No. 0.02;

80.3%; 90.9%;

1; Indels

0; Mismatches

```
The present sequence is a specific example of claimed immunogenic peptides having a sequence from hPTH(1-37) which includes the N- or C-terminal alpha-helical region and/or the non-structured region of the hormone. Antibodies and their binding fragments generated by injecting an animal with the peptides are useful as diagnostic reagents for determination of biologically active hPTH(1-37)
 The present sequence represents a parathyroid hormone (pTH) fragment, comprising amino acids 1-10. Parathyroid hormone fragments of the invention have lipolysis stimulating activity (especially when topically administered). The lipolytic activity of the peptides is enhanced when they are chemically modified to increase their lipophilicity. The peptides are used in cosmetic or dermatological compositions for skin care. They are especially used for slimming treatment of excessive weight in the thighs and hips, in the treatment of cellulite and for skin
 New parathyroid hormone fragment peptides, used as lipolysis stimulants in topically applied cosmetic compositions for slimming treatment of excessive weight in hips and thighs.
 Gaps
 Parathyroid hormone; lipolysis; cosmetic; dermatological; skin care; slimming treatment; cellulite; skin firming.
 ..
 Length 10;
 Score 42; DB 3; Length 10;
Pred. No. 0.37;
1; Mismatches 1; Indels
 1; Indels
 Amino acids 1-10 of a parathyroid hormone (pTH).
 DB 2;
 Score 42; DB 2;
Pred. No. 0.37;
 Mismatches
 AAY68767 standard; peptide; 10 AA.
 Claim 1; Page 8; 18pp; French.
 68.9%;
 68.9%;
80.0%;
 99WO-FR001687.
 98FR-00009193.
 Best Local Similarity 80.0
Matches 8; Conservative
 Query Match
Best Local Similarity 80.0
Matches 8; Conservative
 10
 10
 1 AVSEIQFMHN 10
 1 AVSEIQFMHN
 1 SVSEIQLMHN
 SVSEIQLMHN
 WPI; 2000-171243/15
 Sequence 10 AA;
 WO200004047-A1.
 (SEDE-) SEDERMA
 Sequence 10 AA;
 17-JUL-1998;
 07-JUL-1999;
 Unidentified
 05-MAY-2000
 27-JAN-2000
 Lintner K;
 AAY68767;
 Query Match
 RESULT 5
 8888888888
 à
 ò
 Db
 ô
 Gaps
 hormone; hPTH; antigen; alpha-helix; immunogen;
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0
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Maegerlein M;

Hock D,

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Fusion peptide; tat; hPTHDP; parathyroid hormone; skin; cosmetic;
lipolysis; human; hPTH.
 parathyroid hormone (hPTH) fragment (residues 1-10).
(first entry)
 WO2003035697-A1
 Sequence 10 AA;
04-AUG-2003
 Homo sapiens.
 09-FEB-2000
 01-MAY-2003
 AAY50600;
 Song Y,
Chang M;
 Human
 AAY50600
 RESULT
 Dp
à
 This invention describes a novel method for determining (MI) the content of active parathyroid hormone (A) by treating a sample with (I) antibody (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A), and including the N-terminal residue and (ii) antibody (Ab2) that recognizes an epitope within the receptor-binding site of (A). The number of molecules that react with both antibodies is determined and used to calculate the content of physiologically active (A). The method is used for diagnosis of calcium-metabolism disorders, osteopathy, or hypo- or hyper-parathyroidism. The method (unlike known assays) recognizes that (I) some fragments of (A) shorter than the complete (B4 aa) peptide are active and (ii) that apparently intact peptide may be biologically active and (ii) that apparently intact peptide may be biologically active and (ii) these have the receptor-binding site but lack the N-terminus). It thus provides a true measure of the content of physiologically active (A); contrast methods that measure intact peptide and its 1-37 fragment which may produce falsely high values. This choice is a peptide fragment used to illustrate the method of
 ö
 Determining the content of physiologically active parathyroid hormone, useful in diagnosis of calcium-metabolism disorders, using two antibodies reactive with different epitopes.
 Gaps
 Parathyrold hormone; hPTH; immunogenic peptide; human; epitope; diagnosis; calcium-metabolism disorder; osteopathy; antagonist; hypo-parathyroldism; hyper-parathyroldism.
 .
 68.9%; Score 42; DB 4; Length 10; 80.0%; Pred. No. 0.37; 1; Indels ive 1; Mismatches 1; Indels
 Human parathyroid hormone immunogenic peptide SEQ ID 1.
 AAB86219 standard; peptide; 10 AA.
 Disclosure; Page 3; 10pp; German.
 99DE-01061350.
 99DE-01061350
 (IMMU-) IMMUNDIAGNOSTIK AG.
 (first entry)
 Conservative
 1 AVSEIQFMHN 10
 WPI; 2001-376318/40.
 Local Similarity
nes 8; Conser
 Sequence 10 AA;
 Armbruster FP;
 DE19961350-A1
 03-SEP-2001
 Homo sapiens.
 17-DEC-1999;
 17-DEC-1999;
 21-JUN-2001
 AAB86219;
 Query Match
 Matches
 RESULT 6
AAB86219
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ABR44166 standard; peptide; 10 AA.

RESULT 7 ABR44166 ABR44166;

SVSEIQLMHN 10

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Novel fusion peptide comprising self cell-penetrating Tat peptide bound to human parathyroid hormone-derived peptide, useful as component of skin slimming cosmetic composition.
 The invention relates to a fusion peptide (Tat-hPTHDP), where self cellpenetrating Tat peptide is bound to human parathyroid hormone-derived peptide (hPTHDP). The fusion peptide is useful as a component of skin slimming cosmetic composition. The fusion peptide does not cause irritation, easily and safely penetrates into integument and endothelium, does not cause skin disease and has superior lipolysis effects, and is durable. The present sequence represents a human parathyroid hormone (hPTH) fragment that can be used to construct the fusion peptide
 Cyclic peptide; resin bound; parathyroid hormone; osteopathic; disease; hypotensive; PTH receptor; treatment; hypot-adloemia; osteoporosis; osteopenia; hypot-parathyroidism; hypo-parathyroidism; cushing's syndrome; renal failure; hypottension; bone fracture repair.
 Gaps
 Min H;
 ;
 Lim J,
 Length 10
 1; Indels
 Lee Y,
 Score 42; DB 6;
Pred. No. 0.37;
1; Mismatches
 Cho W, Kang S,
 (GLDS) LG HOUSEHOLD & HEALTH CARE LTD.
 Location/Qualifiers
 /note= "Ser(OtBu)"
 AAYS0600 standard; peptide; 11 AA
 'note= "FMOC-Ala"
 Claim 5; Page 6; 32pp; English
 Resin bound cyclic peptide 33.
06-MAY-2002; 2002WO-KR000835.
 27-SEP-2001; 2001KR-00060245.
15-MAR-2002; 2002KR-00014062.
 68.9%;
80.0%;
 (first entry)
 Kang N, Park S,
 Query Match
Best Local Similarity 8v...
8; Conservative
 SVSEIQLMHN 10
 WPI; 2003-468288/44.
 1 AVSEIQFMHN
 Misc-difference 3
 Misc-difference
 Synthetic.
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This invention describes a novel method for determining (MI) the content of active parathyroid hormone (A) by treating a sample with (i) antibody (Ab) that recognizes the epitope formed by amino acids (aa) 1-3 of (A), and including the N-terminal residue and (ii) antibody (Ab2) that recognizes an epitope within the receptor-binding site of (A). The number of molecules that react with both antibodies is determined and used to calculate the content of physiologically active (A). The method is used for diagnosis of calcium-metabolism disorders, osteopathy, or hypo-or hyper-parathyroidism. The method (unlike known assays) recognizes that (i) some fragments of (A) shorter than the complete (84 aa) peptide are active and (ii) that apparently intext peptide may be biologically are antagonistic (these have the receptor-binding site but lack the N-terminus). It thus provides a true measure of the content of the reminus of the content of the child single and the income represents a peptide fragment used to illustrate the method of the income represents a peptide fragment used to illustrate the method of
 Determining the content of physiologically active parathyroid hormone, useful in diagnosis of calcium-metabolism disorders, using two antibodies reactive with different epitopes.
 Parathyroid hormone peptide, PTH, PTH-related peptide, PTHrP; calcium homeostasis, PTH-1 receptor, PTH-2, vitamin D synthesis; bone synthesis, agonist, osteoporosis, non-parenteral delivery.
 Score 41; DB 4; Length 9;
Pred. No. 1.4e+06;
); Mismatches 1; Indels
 PTH(1-14)/PTHrP(1-14)-derived peptide, SEQ ID NO:6.
 AAB01862 standard; peptide; 9 AA.
 Disclosure; Page 3; 10pp; German
 .
 67.2%;
88.9%;
 99DE-01061350
 99DE-01061350
 (IMMU-) IMMUNDIAGNOSTIK AG.
 11-SEP-2000 (first entry)
 Query Match
Best Local Similarity 85..
8, Conservative
 5
 WPI; 2001-376318/40.
 2 VSEIOFMHN
 1 VSEIOLMHN
 WO200023594-A1.
 Sequence 9 AA;
 Armbruster FP;
 DE19961350-A1
 the invention
 17-DEC-1999;
 17-DEC-1999;
 20-OCT-1999;
 21-JUN-2001.
 27-APR-2000.
 Synthetic.
 AAB01862;
 RESULT 10
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 g
 This invention describes a novel method for the preparation of peptides (II) that contain both cyclic and linear peptide fragment comprises sequential reaction of a result-bound linear fragment with the cyclic sequential reaction of a result optionally other linear fragment. The cyclic and optionally other linear fragments. The products of the invention have osteopathic and hypotensive activity. (II) bind to hPTH receptors and act as agoinsts or antagonists of hPTH. The method is particularly used to prepare cyclic peptide analogs of parathyroid hormone (PTH) or PTH-related peptides which are useful for receptors (with or without activation of adenyly) cyclase activity), e.g. hyper- or hypo-calcemia, osteoporosis, osteopenia, hyper- or hypo-calcemia, osteoporosis, osteopenia, hyper- or hypo-calcemia, syndrome, renal failure and hypertension, also parathyroidism, Cushing's syndrome, renal failure and hypertension, also fragment allows convergent synthesis of result-bound (II), with better yields and higher throughput. The difficulties associated with can be purified before reaction with the resin-bound component. AAY50568-1005614 represent the peptide fragments described in the method of the
 ij
 Gaps
 Convergent synthesis of peptides for treating e.g. bone disorders
 Η,
 Parathyroid hormone; hPTH; immunogenic peptide; human; epitope; diagnosis; calcium-metabolism disorder; osteopathy; antagonist; hypo-parathyroidism; hyper-parathyroidism.
 Score 41.5; DB 2; Length 11; Pred. No. 0.5; 0; Indels 1; Mismatches 0; Indels
 Human parathyroid hormone immunogenic peptide SEQ ID 7.
 (RHON) RHONE-POULENC RORER PHARM INC
 Disclosure; Page 75; 85pp; English.
 /note= "Glu(OtBu)
 note= "Gln(Trt)"
 'note= "His(Trt)"
 /note= "Asn(Trt)"
 AAB86225 standard; peptide; 9 AA.
 99WO-US008435
 98US-0081897P.
 ch 68.0%;
1 Similarity 83.3%;
10; Conservative :
 (first entry)
 1 AVSEIGFMHNLG 12
 Sledeski AW, Mencel JJ;
 WPI; 1999-633822/54.
 Query Match
Best Local Similarity
Matches 10; Conserv
Misc-difference 4
 Misc-difference
 Misc-difference
 Misc-difference
 Sequence 11 AA;
 15-APR-1998;
 15-APR-1999;
 WO9952933-A1
 03-SEP-2001
 21-OCT-1999
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Invention

AAB86225;

AAB86225

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Gaps

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bone reformation; resorption; remodeling; tether1; osteoporosis

99WO-US031108

0-DEC-1999;

06-JUL-2000.

WO200039278-A2.

Homo sapiens.

Jueppner H;

98US-0105530P.

22-OCT-1998;

```
PTH; parathyroid hormone; N-terminal; signaling domain; bone mass;
 Parathyroid hormone N-terminal signaling domain (residues 1-9).
 Potts JT, Jueppner H;
 0; Mismatches
 Disclosure; Page 26; 73pp; English
 AAY96966 standard; peptide; 9 AA.
 PTH-1/PTH-2 receptor agonists
 Gardella TJ, Kronenberg HM,
 Best Local Similarity 88.8
Matches 8; Conservative
 GARD/) GARDELLA T J.
KRON/) KRONENBERG H M.
POTT/) POTTS J T.
 1 AVSEIQFMH 9
 1 AVSEIQLMH 9
 WPI; 2000-339693/29
 JUEPPNER H.
 Sequence 9 AA;
 31-OCT-2000
 AAY96966;
 Query Match
 JUEP/)
 8
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Compounds of the structure or formula S-(L) n-B, R l-S-(L) n-R or S-(L) n-R, are new, S is an amino terminal signaling functional domain of parathyroid hormone (PTH); L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4); B is a C-terminal binding portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R l is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor sequence. The new compounds are used for treating mammalian conditions reformation, bone resorption and/or bone reformation, none resorption and/or bone remodeling, treating diseases and disorders associated with decreased tetherl activity, increasing cAMP in a mammalian cell having PTH-1 receptors, or screening for a peptide or non-peptide PTH (claimed). The new compound can be administered by inhalation unlike the large native PTH or PTH:P which avoids the need for regular injections to treat osteoporosis
 linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass.
 New compound comprising an amino terminal signaling functional domain
 Kronenberg HM, Potts JT,
 Claim 4; Page 92; 119pp; English.
 98US-0114577P.
 (GARD/) GARDELLA I J. (KRON/) KRONENBERG H M. (POTIT/) POTIS J I. (JUEPP) JUEPPNER H.
 WPI; 2000-452384/39
 Sequence 9 AA;
 31-DEC-1998;
 Bardella TJ,
 06-NOV-1996
 AAR91645;
 Query Match
 RESULT 12
 AAR91645
à
 g
 The invention relates to a novel parathyroid hormone (PTH) peptide

(AAB01859) and parathyroid hormone-related peptide (PTHrP; AAB01860), and

bologically active derivatives thereof (AAB01850, AAB01860), and

bologically active derivatives thereof (AAB01850, AAB01860), and

BOLOGICALLY active derivatives thereof (AAB01850, AAB01860), and

CC BOLUSSO, The peptides of the invention are at least 85% identical to the

CC GIV-LYS-KG (AAB01857) where: XI is Ser or Alai X2 is lie or LYS; X6

CG IV-LYS-KG (AAB01857) where: XI is Ser or Alai X2 is lie or LYS; X3 is

CC GIV-LYS-KG (AAB01857) where: XI is Ser or Alai X2 is lie or LYS; X6

CC INVENTION also encompass fragments of peptides of the invention

CC consisting of amino acids 1-9, 1-10, 1-11, 1-12 and 1-13, and N- and C-

CC invention also encompass fragments of peptides of the invention

CC and is necessary for the normal function of the gastrointestinal,

CC and is necessary for the normal function of the gastrointestinal,

CC and is necessary for the normal function of the gastrointestinal,

CC and is necessary for the normal function of the gastrointestinal,

CC and is necessary for the normal function of the gastrointestinal,

CC and is necessary for the normal function of the gastrointestinal,

CC and is necessary for the normal function of the gastrointestinal,

CC and is necessary for the normal function of the graph and is necessary for the normal vitamin of properties on osteoblasts and renal tubular cells,

CC phosphate clearance and vitamin D Synthesis in the kidney. A homologous

CC phosphate clearance and vitamin D Synthesis in the kidney. A homologous

CC calls of protein hormones, the PTH-1 receptor. The peptides of the

CC invention and skeletal actions of PTH-1 and PTH-2 receptors antagonists (AAB01867-

CC conditions are either agonises are useful for the treatment of

CC conditions characterised by a decrease in horm mass, such as

CC conditions characterised by a decrease in horm

CC and/or bone remodelling in a patient. The peptides of the in
 ö
 Parathyroid hormone (PTH) peptides, PTH related peptides and the nucleic acids that encode them, useful for treating osteoporosis.
 Gaps
 .
0
 63.9%; Score 39; DB 3; Length 9; 88.9%; Pred. No. 1.4e+06;
 1; Indels
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Gaps
 Human parathyroid hormone; hPTH; antigen; alpha-helix; immunogen; diagnosis; active hPTH 1-37.
 ·,
Score 39; DB 3; Length 9;
Pred. No. 1.4e+06;
0; Mismatches 1; Indels
 Human parathyroid hormone antigenic peptide hPTH 1-9.
 0; Mismatches
 AAR91645 standard; peptide; 9 AA
 94DE-04434551.
 63.9%;
 (first entry)
 Best Local Similarity 88.9
Matches 8, Conservative
 1 AVSEIQLMH 9
 1 AVSEIQEMH 9
 28-SEP-1994;
 DE4434551-A1
 04-APR-1996.
 Synthetic
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.. 0

us-09-730-174a-6.closed.rag

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CC (AAB01859) and parathyroid hormone-related peptide (PTHTP; AAB01860), and biologically active derivatives thereof (AAB01857-B01858, AAB01861).

CC bols69. The peptides of the invention are at least 5% identical to the generic peptide of the formula: X1-Yal-Sex-Glu-X2-Glu-Leu-X3-His-X4-X5-CG Gly-Lyes (AAB01857) where: X1 is Ser or Ala; X2 is Ile or Lys; X3 is provided that the peptide is no APP; X5 is Leu or Lys; X6 is His or Ser; provided that the peptide is no PTHTP(1-14). The peptides of the provided that the peptide is no PTHTP(1-14). The peptides of the invention also encompass fragments of peptides of the invention consisting of amino acids 1-9, 1-10, 1-11, 1-12 and 1-13, and N- and C- terminal derivatives. PTH is a major regulator of calcium homeostasis, and is necessary for the normal function of the gastrointestinal, sheletal, neurological system, neuromuscular and cardiovascular systems. It binds to both PTHT-1 receptors on soteoblasts and renal tubular cells, and to the recently identified PTH-2 receptor. PTH has a potent anabolic effect on the skeleton, and mediates calcium reabsorption, enhances proceed to the recently identified PTH-2 receptor. PTH has a potent anabolic celfect on the skeleton, and mediates calcium reabsorption, enhances proceed and vitemin D synthesis in the kidney. A homologous calls of protein hormones, the PTH-related proteins (PTH-P) mimic some of the renal and skeletal actions of PTH-1 and also bind to the PTH-1 receptor angonists of PTH-2 receptor. They peptides of the invention are also cateoporosis. PTH-1/PTH-2 receptor antagonists are useful for treatment of conditions characterised by a decrease in bone mass, such as condition and care and proceed and/or bone remodelling in a patient. The peptides of the invention are also contectors. PTH-2 receptor antagonists are useful for the determination of rates of bone formation, bone remodelling in a patient. The peptides of the invention are entered "minimised" versions of PTH-1 which are inexpensive to prepare the period an
 PTH; parathyroid hormone; N-terminal; signaling domain; bone mas
bone reformation; resorption; remodeling; tetherl; osteoporosis.
 ..
0
 59.0%; Score 36; DB 3; Length 9; 77.8%; Pred. No. 1.46+06; ive 1; Mismatches 1; Indels
 Ä
 Jueppner
 Parathyroid hormone N-terminal signaling domain.
 Potts JT,
 AAY96981 standard; peptide; 9 AA.
 Gardella TJ, Kronenberg HM,
 99WO-US031108
 98US-0114577P
 (first entry)
 GARDELLA T J.
KRONENBERG H M.
POTTS J T.
JUEPPNER H.
 | | | | | | : |
1 AVSEIQLLH
 1 AVSEIQFMH
 WO200039278-A2.
 Sequence 9 AA;
 30-DEC-1999;
 Homo sapiens
 31-DEC-1998;
 31-OCT-2000
 06-JUL-2000
 AAY96981;
 (KRON/)
(POTT/)
(JUEP/)
 (GARD/)
 RESULT 14
 AAY96981
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 The present sequence is a specific example of claimed immunogenic peptides having a sequence from hPTH(1-37) which includes the N- or C-terminal alpha-helical region and/or the non-structured region of the hormone. Antibodies and their binding fragments generated by injecting an animal with the peptides are useful as diagnostic reagents for determination of biologically active hPTH(1-37)
 New antigenic peptide(s) from human parathyroid hormone - and antibodies generated using them, able to distinguish between active and inactive forms of the hormone.
 Parathyroid hormone (PTH) peptides, PTH related peptides and the nucleic acids that encode them, useful for treating osteoporosis.
 Gaps
 The invention relates to a novel parathyroid hormone (PTH) peptide
 Parathyroid hormone peptide; PTH; PTH-related peptide; PTHrP; calcium homeostasis; PTH-1 receptor; PTH-2; vitamin D synthesis; bone synthesis; agonist; osteoporosis; non-parenteral delivery.
 ;
0
 Score 36; DB 2; Length 9;
Pred. No. 1.4e+06;
1; Mismatches 1; Indels
 Jueppner H;
 PTH(1-14)/PTHrP(1-14)-derived peptide, SEQ ID NO:7.
 Maegerlein M;
 Potts JT,
 Ď,
 Disclosure; Page 26; 73pp; English
 AAB01863 standard; peptide; 9 AA
 Hock
 Gardella TJ, Kronenberg HM,
 Claim 2; Page 4; 5pp; German.
 Query Match 59.0%;
Best Local Similarity 77.8%;
Matches 7; Conservative 1
 94DE-04434551
 99WO-US024481
 98US-0105530P
 3
 (first entry)
 (GARD/) GARDELLA T J.
(KRON/) KRONENBERG H M.
(POTI/) POTIS J T.
(JUEP/) JUEPPNER H.
 Forssmann
 :||||| ||
1 SVSEIQLMH 9
 1 AVSEIQFMH 9
 (FORS/) FORSSMANN W.
 WPI; 1996-180391/19.
 WPI; 2000-339693/29
 Sequence 9 AA;
 WO200023594-A1
 28-SEP-1994;
 20-0CT-1999;
 sapiens
 22-OCT-1998;
 Adermann K,
 11-SEP-2000
 27-APR-2000.
 Synthetic.
 AAB01863;
 Ношо
 RESULT 13
 AAB01863
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Gaps

WPI; 2000-452384/39.

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DE19961350-A1.
 17-DEC-1999;
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Compounds of the structure or formula S-(I) n-B, R.1-S-(I) n-R or S-(I) n-R, are new, S is an amino terminal signaling functional domain of parathyroid hormone (PTH); L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4); B is a C-terminal binding portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor sequence in the new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone. Teformation, bone resorption and/or bone remodeling, treating diseases and disorders associated with decreased tetherl activity, increasing cAMP in a mammalian cell having PTH-1 receptors, or screening for a peptide or non-peptide PTH (claimed). The new compound can be administered by inhalation unlike the large native PTH or PTH:PP which avoids the need for regular injections to treat osteoporosis
New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass.
 Claim 11; Page 93; 119pp; English
 Sequence 9 AA;
```

Gaps ; 0 Score 36; DB 3; Length >;
Pred. No. 1.4e+06; 1; Mismatches 59.0%; Query Match
Best Local Similarity 77.6
Matches 7; Conservative σ σı SVSEIQLMH 1 AVSEIOFMH

AAB86220 standard; peptide; 9 AA. (first entry) 03-SEP-2001 AAB86220;

Parathyroid hormone; hPTH; immunogenic peptide; human; epitope; diagnosis; calcium-metabolism disorder; osteopathy; antagonist; hypo-parathyroidism; hyper-parathyroidism. Human parathyroid hormone immunogenic peptide SEQ ID 2.

21-JUN-2001..

99DE-01061350 17-DEC-1999; 99DE-01061350 (IMMU-) IMMUNDIAGNOSTIK AG.

Armbruster FP;

WPI; 2001-376318/40.

Determining the content of physiologically active parathyroid hormone, useful in diagnosis of calcium-metabolism disorders, using two antibodies reactive with different epitopes.

This invention describes a novel method for determining (M1) the content of active parathyroid hormone (A) by treating a sample with (i) antibody Disclosure; Page 3; 10pp; German.

cand including the N-terminal residue and (ii) antibody (Ab2) that
cand including the N-terminal residue and (ii) antibody (Ab2) that
coordiales an epitope within the receptor-binding site of (A). The number
of molecules that react with both antibodies is determined and used to
calculate the content of physiologically active (A). The method is used
for diagnosis of calcium-metabolism disorders, osteopathy, or hypoc for diagnosis of calcium-metabolism disorders, osteopathy, or hypoc hyper-parathyroidism. The method (unlike known assays) recognizes that
c hyper-parathyroidism. The method (unlike known assays) recognizes that
c in some fragments of (A) shorter than the complete (84 aa) peptide are
active and (ii) that apparently intact peptide may be biologically
are antagonistic (these have the receptor-binding site but lack the Nterminus). It thus provides a true measure of the content of
physiologically active (A); contrast measure intact peptide
and its 1-37 fragment which may produce falsely high values. This
sequence represents a peptide fragment used to illustrate the method of the invention 

Sequence 9 AA;

Gaps ., 0 Score 36; DB 4; Length 9; Pred. No. 1.4e+06; 1; Mismatches 1; Indels 59.0%; Query Match
Best Local Similarity 77.8
Matches 7; Conservative

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σ 1 AVSEIQFMH à

1 SVSEIQLMH d

5, 2004, 09:34:31 Search completed: September Job time : 37.5 secs

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99; Search time 32.5 Seconds (without alignments) 116.332 Million cell updates/sec
 Published Applications AA:*

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6: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
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5.1.6
Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 1298764 segs, 315065143 residues
GenCore version
Copyright (c) 1993 - 2004
 5, 2004, 09:37:09
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 BLOSUM62
Gapop 10:0 , Gapext 0.5
 US-09-730-174A-6
61
1 AVSEIQFMHNLG 12
 September
 Minimum DB seq length: 0 Maximum DB seq length: 12
 score:
 Scoring table:
 Database :
 Sequence:
 Searched:
 Title:
Perfect :
 Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|             | Description | quenc            | 4                | 7                | 'n               | Sequence 3, Appli | H                | -               | Sequence 7, Appli | 9               | œ               | ,               | Sequence 2, Appli | 8                 | m                 | 60              |
|-------------|-------------|------------------|------------------|------------------|------------------|-------------------|------------------|-----------------|-------------------|-----------------|-----------------|-----------------|-------------------|-------------------|-------------------|-----------------|
| SUMMARIES   | QI          | US-09-730-174A-6 | US-09-730-174A-4 | US-09-730-174A-2 | US-09-730-174A-5 | US-09-730-174A-3  | US-09-730-174A-1 | US-10-168-185-1 | US-10-168-185-7   | US-10-192-673-6 | US-10-168-185-8 | US-10-192-673-7 | . US-10-168-185-2 | . US-10-192-673-8 | . US-10-168-185-3 | US-10-232-187-8 |
|             | Length DB   | 12 9             | 12 9             | 11 9             | 12 9             | 12 9              | 11               | 10 14           | 9 14              | 9 14            | 8 14            | 9 14            | 9 14              | 9 14              | 8 14              | 10 14           |
| .*<br>Query | Match       | 100.0            | 95.1             | 93.4             | 90.2             | 85.2              | 83.6             | 68.8            | 67.2              | 63.9            | 60.7            | 59.0            | 59.0              | 47.5              | 45.9              | 44.3            |
|             | Score       | 61               | 28               | 57               | 52               | 52                | 51               | 42              | 41                | 39              | 37              | 36              | 36                | 29                | 28                |                 |
| Result      | No.         | н                | 63               | ო                | 4                | ហ                 | φ                | 7               | 00                | σ               | 10              | 11              | 12                | 13                | 14                | 15              |

| Sequence 2, Appli | Sequence 10, Appl | 4            | e 4.         | equence 12  | 9               | 4             | Н          | e 1               | 1                 | 9              | 4                 | 4             | ь<br>Б   | equence 5        | (a)   | equence 1      | equence 13       | 45,             | 55,         | 73,           | e 78,    | 26,         | e 61             | e 14             | e 93             | e 16     | o,               | 4        | a)             |
|-------------------|-------------------|--------------|--------------|-------------|-----------------|---------------|------------|-------------------|-------------------|----------------|-------------------|---------------|----------|------------------|-------|----------------|------------------|-----------------|-------------|---------------|----------|-------------|------------------|------------------|------------------|----------|------------------|----------|----------------|
| 5 US-10-366-7     | 4 US-10-19        | US-09-976-78 | US-09-865-19 | US-09-965-0 | 0 US-09-563-222 | 9-864-60-SD 0 | 2 US-10-23 | 3 US-10-051-852-1 | 4 US-10-195-752-1 | 4 US-10-160-23 | 4 US-10-160-232-1 | 4 US-10-283-3 | 4 US-10- | 5 US-10-137-867- | 5     | 5 US-10-430-17 | 1 US-09-791-551- | US-09-834-765-4 | US-09-834-7 | -09-834-765-7 | US-09-83 | US-09-910-0 | 4 US-10-033-741- | 4 US-10-153-334- | 5 US-10-391-364- | 4 US-10- | 4 US-10-168-185- | 4 US-10- | 4 US-10-043-48 |
|                   |                   |              |              | 0           | 0               | 0             | 0          | 0                 | 0                 | 0              | 0                 | 0             | 0        | 0                | 0     |                | н                |                 |             | 0             | 0        | 0           | 0                | -                |                  | 2        |                  |          |                |
| 7 44.             | 6 42.             | 5 41.        | 5 41.        | 5.44        | 5 41.           | 5 .41.        | 5          | 5 41.             | 5 41.             | 5 41.          | 5                 | 5 41.         | 5 41.    | 5 4              | 5 41. | 5              | 5 41.            | 4 39.           | 4 39.       | 4 39.3        | 4 39.    | 39.         | 4 39.            | 4 39.            | 4 39.            | 4 39.    | 3 37.            | 3 37.    | 3 37.          |
| 6                 | 7                 | 8            | 9            | 0           | 1 2             | 2             | 3          | 4                 | 5                 | 9              | 7 2               | 8             | 9        | 0                | 1 2   | 7              | 3 2              | 7               | 73          | 36 2          | 7        | 7           | 9                | (1)              | 0                | 7        | 7                | 2        | 45 2           |

# ALIGNMENTS

```
Sequence 6, Application US/09730174A

Batent No. US20020110871A1

GENERAL INFORMATION:

TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having

TITLE OF INVENTION: Selective Binding Specificity to Bloactive Intact Parathyroid H

CURRENT APPLICATION NUMBER: US/09/730,174A

NUMBER OF SEQ ID NOS: 12

SEQ ID NO 6: 12

ENGTH: 12
 Sequence 4, Application US/09730174A

Patent No. US20020110871A1

GENERAL INFORMATION:
APPLICANT: Zahradnik, R.J.
TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having (TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid He
 OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies US-09-730-174A-6
 ó
 Gaps
 .;
0
 Length 12
 Indels
 ;
0
 Score 61; DB 9;]
Pred. No. 0.00014;
 0; Mismatches
 Query Match
Best Local Similarity 100.0%;
Matches 12; Conservative 0
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 1 AVSEIQFMHNLG 12
RESULT 1
US-09-730-174A-6
 RESULT 2
US-09-730-174A-4
 TYPE: PRT
 FEATURE:
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Sequence 3, Application US/09730174A

Sequence 3, Application US/09730174A

Sequence 3, Application US/0973017AI

GREERL NO. US2002011087AI

GREERL NO. US200201108:

TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Ho. TITLE OF INVENTION: NUMBER: US/09/730,174A

CURRENT FILING DATE: 2000-12-05

NUMBER OF SEQ ID NOS: 12

SEQ ID NO 3

LENGTH: 12
 Squence 1, Application US/09730174A
Patent No. US2020110871A1
GENERAL INFORMATION:
PAPLICANT: Zahradaik, R.J.
TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid HO
FILE REFERENCE: IMUNE-001A
CURRENT APPLICATION NUMBER: US/09/730,174A
NUMBER OF SEQ ID NOS: 12
 ; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies US-09-730-174A-1
 , OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies US-09-730-174A-3
 ;
0
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 Gaps
 Gaps
 ..
 .;
0
 Length 11;
 Length 12;
 Score 52; DB 9; Length 12;
Pred. No. 0.0063;
1; Mismatches 1; Indels
 1; Indels
 Sequence 1, Application US/10168185
Publication No. US20030175802A1
SEPREAL INFORMATION:
APPLICANT: Ambruster, Franz Paul
APPLICANT: Missbichler, Albert
APPLICANT: Schmidt-GaYX, Heinrich
APPLICANT: Schmidt-GaYX, Heinrich
APPLICANT: Schmidt-GaYX, Heinrich
APPLICANT: Noth, Heinz-Jurgen
TITLE OF INVENTION: Method for Determining Parathormone
 Best Local Similarity 90.9%; Pred. No. 0.00089; Matches 10; Conservative 0; Misman-L
 Query Match

Best Local Similarity 83.3%;

Matches 10; Conservative
 TYPE: PRT
ORGANISM: Artificial Sequence
 ORGANISM: Artificial Sequence
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 RESULT 5
US-09-730-174A-3
 RESULT 6
US-09-730-174A-1
 RESULT 7
US-10-168-185-1
 SEQ ID NO 1
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 Sequence 5, Application US/09730174A

Sequence 5, Application US/09730174A

Sequence 5, Application US/09730174A

GENERAL INFORMATION

APPLICANT: Zahradnik, R.J.

TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid HG

FILE REFERENCE: IMUNDER: US/09/730,174A

CURRENT PPLICATION NUMBER: US/09/730,174A

NUMBER OF SEQ ID NOS: 12

LENGTH: 12
 Sequence 2, Application US/09730174A

Patent No. US20020110871A1

GENERAL INFORMATION:

APPLICANT: Zahradnik, R.J.

TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid HG FILE REFERENCE: IMMUNE 001A

CURRENT FILING DATE: 2000-12-05

NUMBER OF SEQ ID NOS: 12
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 ; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-4
 , OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies US-09-730-174A-2
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 Length 12;
 Score 58; DB 9; I
Pred. No. 0.00049;
1; Mismatches 0;
 CURRENT APPLICATION NUMBER: US/09/130,174A CURRENT FILING DATE: 2000-12-05 SEQ ID NOS: 12 SEQ ID NO 4
 95.1%;
91.7%;
 TYPE: PRT
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 TYPE: PRT ORGANISM: Artificial Sequence
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 1 AVSEIQFMHNLG 12
 2 VSEIOFMHNLG 12
 1 VSEIOFMHNLG 11
 Query Match
Best Local Similarity
 RESULT 3
US-09-730-174A-2
 RESULT 4
US-09-730-174A-5
 SEQ ID NO 2
LENGTH: 11
 FEATURE:
 LENGIH:
 Matches
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Gaps

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Sequence 7, Application US/10192673
Publication No. US20303166838A1
GENERAL INFORMATION:
APPLICANT: Gardella, Thomas J.
APPLICANT: Knoemberg, Henry
APPLICANT: Foreinberg, Henry
APPLICANT: Juppner, Harald
TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
TITLE OF INVENTION: Hormone-Related Peptide (PTHrp)
 OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: peptide
 Score 39; DB 14; Length 9;
Pred. No. 1.2e+06;
0; Mismatches 1; Indels
 APPLICANT: Armbuser, Franz Paul
APPLICANT: Armbuser, Franz Paul
APPLICANT: Armbuser, Albert
APPLICANT: Schmidt-Gayk, Heinrich
APPLICANT: Schmidt-Gayk, Heinrich
APPLICANT: Roth, Heinz-Jurgen
TITLE OF INVENTION: Method for Determining Parathormone;
TITLE OF INVENTION: Activity in a Human Sample
FILE REFERENCE: HLZ-004US
CURRENT APPLICATION NUMBER: US/10/168,185
CURRENT APPLICATION NUMBER: PCT/EP00/12911
PRIOR FILING DATE: 2000-12-18
PRIOR FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 11
SEQ ID NOS: 11
LENGTH: 8
LENGTH: 8
 60.7%; Score 37; DB 14; Length 8; 87.5%; Pred. No. 1.2e+06; tive 0; Mismatches 1; Indels
 CURRENT APPLICATION NUMBER: US/10/192,673
CURRENT FILING DATE: 2002-07-11
PRIOR APPLICATION NUMBER: U.S. 09/421,379
PRIOR FILING DATE: 1999-10-20
PRIOR FILING DATE: 1998-10-22
NUMBER OF SEQ ID NOS: 13
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 6
 Sequence 8, Application US/10168185; Publication No. US20030175802A1; GENERAL INFORMATION:
 ·,
 63.9%;
88.9%;
 TYPE: PRT ORGANISM: Artificial Sequence
 Query Match
Best Local Similarity 88.5
Matches 8; Conservative
 Conservative
 TYPE: PRT; ORGANISM: Homo sapiens
US-10-168-185-8
 1 AVSEIQFMH 9
 1 AVSÉIQLMH 9
 SEIOFMHN 10
 1 SEIOLMHN 8
 US-10-192-673-6
 10-192-673-7
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 Db
 엄
 ô
 Gaps
 Sequence 6, Application US/10192673
Publication No. US20030166838A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gradella, Thomas J.
APPLICANT: Kronenberg, Henry
APPLICANT: Potts, John T.
APPLICANT: Unpuprion: Harald
TITLE OF INVENTION: Bloactive Peptides and Peptide Derivatives of TITLE OF INVENTION: Pararhyroid Hormone (PTH) and Parathyroid FITLE OF INVENTION: Hormone-Related Peptide (PTHP)
 ;
 ö
 DB 14; Length 10; 0.38;
 APPLICANT: Asimulatasett, trunc.
APPLICANT: Schmidt-Gayk, Heinrich
APPLICANT: Schmidt-Gayk, Heinrich
APPLICANT: Schmidt-Gayk, Heinrich
APPLICANT: Roth, Heinz-Untgen
TITLE OF INVENTION: Method for Determining Parathormone
TITLE OF INVENTION: Activity in a Human Sample
FILE REPERENCE: HLZ-004US
FILE REPERENCE: HLZ-004US
CURRENT APPLICATION NUMBER: US/10/168,185
CURRENT APPLICATION NUMBER: PCT/EP00/12911
PRIOR FILING DATE: 2000-12-18
PRIOR FILING DATE: 2000-12-18
PRIOR FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 7
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LENGTH: 9
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Pred. No. 1.2e+06;
 1; Indels
 1; Indels
TITLE OF INVENTION: Activity in a Human Sample FILE REFRENCE: HLZ-004US
CURRENT APPLICATION NUMBER: US/10/168,185
CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: PCT/EP00/12911
PRIOR FILING DATE: 2000-12-18
PRIOR FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 10
TYPE: PRIOR FILINGSHIPS
CORCANISM: Homo sapiens
US-10-168-185-1
 1; Mismatches
 Mismatches
 Score 42;
Pred. No.
 Sequence 7, Application US/10168185
Publication No. US20030175802A1
GENERAL INFORMATION:
 APPLICANT: Armbruster, Franz Paul
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 68.9%;
80.0%;
 67.2%;
88.9%;
 Query Match
Best Local Similarity 80.0
Matches 8; Conservative
 Query Match
Best Local Similarity 88.5
Matches 8; Conservative
 1 AVSEIOFMHN 10
 1 SVSEIQLMHN 10
 TYPE: PRT
ORGANISM: Homo sapiens
 2 VSEIQFMHN 10
 1 VSEIQLMHN 9
 RESULT 8
US-10-168-185-7
 US-10-168-185-7
 RESULT 9
US-10-192-673-6
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Gaps

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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
CTHER INFORMATION: peptide
US-10-192-673-8
 Score 29; DB 14; Length 9;
Pred. No. 1.2e+06;
1; Mismatches 2; Indels
Hormone-Related Peptide (PTHrP)
 TITLE OF INVENTION: Hormone-Related Peptide FILE REFERENCE: 06094 4570002
CURRENT APPLICATION NUMBER: 02/10/192,673
CURRENT FILING DATE: 2002-07-11
PRIOR RILING DATE: 1999-10-20
PRIOR FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 9
 APPLICANT: Abrahamson, Julie A.
APPLICANT: Bochner, Bruce
APPLICANT: Brickson-Miller, Connie L.
APPLICANT: Kikly, Kristine K.
APPLICANT: Schleimer, Robert
 Sequence 8, Application US/10232187 Publication No. US20030092091A1 GENERAL INFORMATION:
 Sequence 3, Application US/10168185; Publication No. US20030175802A1; GENERAL INFORMATION: APPLICANT: Armbruseer, Franz Paul
 47.5%;
 Query Match
Best Local Similarity 66.73
Matches 6; Conservative
 Query Match
Best Local Similarity 75.0
Matches 6; Conservative
 TYPE: PRT
ORGANISM: Homo sapiens
 1 AVSEIQFMH 9
 1 AVSEHOLLH 9
 1 AVSEIQFM 8
 RESULT 15
US-10-232-187-8
 RESULT 14
US-10-168-185-3
 US-10-168-185-3
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 Gaps
 Gaps
 Sequence 8, Application US/10192673;
Publication No. US20030166838A1
GENERAL INFORMATION:
APPLICANT: GENERAL Thomas J.
APPLICANT: Kronenberg, Henry
APPLICANT: Potts, John T.
APPLICANT: Juppiner, Harrald
APPLICANT: Juppi
 OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: peptide
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 59.0%; Score 36; DB 14; Length 9; 77.8%; Pred. No. 1.2e+06; tive 1; Mismatches 1; Indels
 APPLICANT: Missbichler, Albert
APPLICANT: Schmidter, Albert
APPLICANT: Schmidter, Heinz-Jurgen
APPLICANT: Schmidter-Gavk, Heinz-Jurgen
TITLE OF INVENTION: Method for Determining Parathormone
TITLE OF INVENTION: Activity in a Human Sample
TITLE OF INVENTION: Activity in a Human Sample
TITLE OF INVENTION: Activity in a Human Sample
CURRENT APPLICATION NUMBER: US/10/168,185
CURRENT FILING DATE: 2000-12-18
PRIOR FILING DATE: 2000-12-18
PRIOR FILING DATE: 1999-12-17
NUMBER: OF SEQ ID NOS: 11
SOFTWARE: FASTERQ for Windows Version 4.0
 Length 9;
 1; Indels
 Score 36; DB 14;
Pred. No. 1.2e+06;
 Mismatches
 FILE REFERENCE: 0609.4570002

CURRENT APPLICATION NUMBER: US110/192,673

CURRENT FILING DATE: 2002-07-11

PRIOR PELICATION NUMBER: U.S. 09/421,379

PRIOR PILING DATE: 1999-10-20

PRIOR APPLICATION NUMBER: U.S. 60/105,530

PRIOR PILING DATE: 1999-10-22

NUMBER OF SEQ ID NOS: 13

SOFURARE: PATENTIN Ver. 2.0

LENGTH: 9
 RESULT 12
US-10-168-185-2
Sequence 2, Application US/10168185
; Publication No. US20030175802A1
; APPLICANT: Armbruster, Franz Paul
 TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
 59.0%;
 Query Match 59.0
Best Local Similarity 77.8
Matches 7; Conservative
 Query Match
Best Local Similarity 77.8
Matches 7; Conservative
 ; ORGANISM: Homo sapiens
US-10-168-185-2
 1 AVSEIQFMH 9
 1 AVSEIQFMH 9
 1 AVSEIQLLH 9
 SVSEIQLMH 9
 RESULT 13
US-10-192-673-8
 US-10-192-673-7
 SEQ ID NO 2
 TYPE: PRT
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0
 Gaps
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0
 45.9%; Score 28; DB 14; Length 8; 75.0%; Pred. No. 1.2e+06;
 1; Indels
APPLICANT: Missbichler, Albert
APPLICANT: Schmidt-Gayk, Heinrich
APPLICANT: Schmidt-Gayk, Heinrich
APPLICANT: Roth, Beinsch
TITLE OF INVENTION: Method for Determining Parathor
TITLE OF INVENTION: Activity in a Human Sample
FILE REFREENCE: HZ-00403
CURRENT APPLICATION NUMBER: US/10/168,185
CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: PCT/EP00/12911
PRIOR APPLICATION NUMBER: DE 19961350
PRIOR FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 8
 1; Mismatches
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APPLICANT: Nulku, Turkan E.

TITLE COF INVENTION: Sialcadhesin Factor-2 Antibodies

FILE REFERENCE: GH50042

CURRENT APPLICATION NUMBER: US/10/232,187

CURRENT FILING DATE: 2000-03-0

PRIOR APPLICATION NUMBER: 60/187,595

PRIOR PELING DATE: 2001-03-03

PRIOR PELING DATE: 2001-03-03

PRIOR PELING DATE: 2001-03-03

PRIOR PELING DATE: 2001-03-03-03

PRIOR PELING DATE: 2001-03-03

PRIOR PELING DATE: 2002-01-18

PRIOR PELING DATE: 2002-07-10

PRIOR PELI
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Search completed: September 5, 2004, 09:49:38 Job time: 32.5 secs

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September 5, 2004, 09:32:03; Search time 11 Seconds (without alignments) 56.319 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 OM protein - protein search, using sw model
 Title:
Perfect score:
Sequence:
 Run on:
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US-09-730-174A-6 61 1 AVSEIQFMHNLG 12

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

389414 segs, 51625971 residues Searched:

121490 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 12

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued Patents AA:\*

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3: /cgn2\_6/ptodata/2/laa/6B\_COMB.pep:\*
4: /cgn2\_6/ptodata/2/laa/PCTUS\_COMB.pep:\*
5: /cgn2\_6/ptodata/2/laa/PCTUS\_COMB.pep:\*
6: /cgn2\_6/ptodata/2/laa/PCTUS\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

|   |        | Description | 31,     | H                | a    | ď                | ۲,       | 54        | ω̈        | 42,        | 'n       | 42,      | e 42,      | e 10,      | 9          | σì      | 97,       | e 12,      | 49,           | 12,           | 12,        | 108        | 49,       | ω          | 56,           | e 56,     | 17,     | Sequence 16, Appl | -           |
|---|--------|-------------|---------|------------------|------|------------------|----------|-----------|-----------|------------|----------|----------|------------|------------|------------|---------|-----------|------------|---------------|---------------|------------|------------|-----------|------------|---------------|-----------|---------|-------------------|-------------|
|   | !      | DI          | -442-98 | US-08-817-547A-1 | 1-3  | US-08-817-547A-2 | -09-421- | 5460978-3 | -09-421-3 | -140-      | -08-817- | -08-482- | -08-482-52 | -09-421-37 | -08-116-77 | -438-56 | -08-483-5 | -08-783-85 | -08-836-561-4 | -09-280-028-1 | -09-344-05 | -09-393-38 | -09-434-1 | -09-091-07 | -08-177-109A- | 08-687-70 | -817-54 | US-08-817-547A-16 | -817-547A-1 |
|   |        | 82          | 4       | 'n               | 4    | ٣                | 4        | 9         | 4         | 7          | ო        | 7        | ო          | 4          | N          | N       | N         | m          | m             | ņ             | 4          | 4          | 4         | 4          | ~1            | N         | ო       | ო                 | ო           |
|   | ٠      | Length      | 12      | 10               | σ,   | σ                | ወ        | 11        | σv        | 12         | œ        | 12       | 12         | 6          | 10         | 10      | 10        | 10         | 10            | 10            | 10         | 10         | 10        | 10         | S             | S         | 5       | 9                 | 7           |
| ф | Query  | Match       | 80.3    | œ.               | 63.9 | φ.               | φ.       | 50.8      |           |            | •        | •        | 44.3       | ď.         | 41.0       | ٠       | ٠         | 41.0       | •             | •             | 41.0       | •          | •         | •          |               | e,        | 39.3    | φ.                | 39.3        |
|   |        | Score       | 4       | 42               |      | 36               |          | 31        |           |            | 28       | 27       | 27         | 26         | 25         | 25      | 25        | 25         | 25            | 25            | 25         | 25         | 25        | 25         | 24            | 24        | 24      | 24                | 24          |
|   | Result | . NO. !     | П       | 7                | m    | 4                | Ŋ        | 9         | 7         | <b>c</b> o | 6        | 10       | 11         | 12         | 13         | 14      | 15        | 16         | 17            | 18            | 19         | 20         | 21        | 22         | 23            | 24        | 25      | 26                | 27          |

| Ann               | 4                   | App      | Appl             | Appl              | Appli           | Appli            | Appl             | Appli           | Appli            | Appli            | Appl             | Appl              | Appl             | Appl              | Appl              | Appli           | Appli           | Appl             |  |
|-------------------|---------------------|----------|------------------|-------------------|-----------------|------------------|------------------|-----------------|------------------|------------------|------------------|-------------------|------------------|-------------------|-------------------|-----------------|-----------------|------------------|--|
| 6.4               |                     | 14,      | 64,              | 13,               | S,              | 7                | 26,              | 'n              | 5                | 4,               |                  |                   | 26,              |                   |                   | m               | 'n              | 83,              |  |
| a Charles         | פאומיייי            | Seguence | Seguence         | Sequence          | Seguence        | Sequence         | Sequence         | Sequence        | Sequence         | Sequence         | Sequence         | Sequence          | Sequence         | Sequence          | Sequence          | Sequence        | Sequence        | Sequence         |  |
| 115-08-748-031-64 | FO : H30 : DF7 : DO |          | US-08-974-297-64 | US-08-817-547A-13 | US-08-432-694-5 | US-08-817-547A-7 | US-09-171-945-26 | US-08-432-694-3 | US-08-817-547A-5 | US-08-817-547A-4 | US-07-822-043-26 | US-08-346-455B-26 | US-08-977-221-26 | US-09-483-831B-26 | PCT-US95-06613-26 | US-09-771-415-3 | US-09-064-750-1 | US-08-615-181-83 |  |
| c                 | 3 (                 | m        | ო                | m                 | Н               | m                | m                | Н               | m                | ო                | Н                | Н                 | m                | 4                 | 'n                | 4               | m               | Н                |  |
| a                 | 0 (                 | œ        | œ                | σn                | 10              | 10               | 10               | 11              | φ                | 7                | σ                | σ                 | σı               | o                 | σ                 | 10              | 12              | 10               |  |
| 30 3              |                     | 39.3     | 39.3             | 39.3              | 39.3            | 39.3             | 39.3             | 39.3            | 37.7             | 37.7             | 37.7             | 37.7              | 37.7             | 37.7              | 37.7              | 37.7            | 37.7            | 36.1             |  |
| 2.4               | 4 4                 | 24       |                  | 24                | . 24            | 24               | 24               | 24              | 23               |                  | 23               | 23                | 23               | 23                | 23                | 23              | 23              | 22               |  |
| ac                |                     | 53       | 30               | 31                | 32              | 33               | 34               | 35              | 36               | 37               | 38               | 39                | 40               | 41                | 42                | 43              | 44              | 45               |  |
|                   |                     |          |                  |                   |                 |                  |                  |                 |                  |                  |                  |                   |                  |                   |                   |                 |                 |                  |  |

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## ALIGNMENTS

| Sequence 31, Application US/09442989  Patent No. 656993  GERERAL INFORMATION: APPLICAN: SIGNESAL INFORMATION: APPLICAN: GENERAL INFORMATION: TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF RESIN-BOUND CYCLIC TITLE OF INVENTION: PROPRIES: TITLE OF INVENTION: PROPRIES: US/09/442,989; CURRENT APPLICATION NUMBER: G6/081,897  GURRENT FILING DATE: 1999-01-18  EARLIER APPLICATION NUMBER: G6/081,897  CURRENT FILING DATE: 1999-04-15  NUMBER OF SOT UN 03.46  SEALLIER APPLICATION NUMBER: G6/081,897  CURRENT FILING DATE: 1999-04-15  NUMBER OF SOT UN 03.46  SOTWARE: PREFITE  LOCATION: (3)  OTHER INFORMATION: FMOC-Ala  PEATURE: NAME/KEY: PEPTIDE  LOCATION: (4)  OTHER INFORMATION: GIU (CDBU)  PEATURE: NAME/KEY: PEPTIDE  LOCATION: (4)  OTHER INFORMATION: GIU (TIC)  PEATURE: NAME/KEY: PEPTIDE  LOCATION: (9)  OTHER INFORMATION: His(TIC)  PEATURE: NAME/KEY: PEPTIDE  LOCATION: (9)  OTHER INFORMATION: His(TIC)  PEATURE: NAME/KEY: PEPTIDE  LOCATION: (9)  OTHER INFORMATION: ASN (TIC)  PEATURE: NAME/KEY: PEPTIDE  LOCATION: (10)  OTHER INFORMATION: Nie  NAME/KEY: ROPENATION: Nie  OTHER INFORMATION: Nie  OTHER INFORMATION: Nie  OTHER INFORMATION: Nie  OTHER INFORMATION: Nie                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | ルージャキーハコーの  | 10-70       |                       |                |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------|-------------|-----------------------|----------------|
| PREPARATION OF RESIN-BOUND 42, 989                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | and the art | 31 Applica  | TS/09442989           |                |
| PREPARATION OF RESIN-BOUND 42,989                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Patent No   | . 656993    |                       |                |
| edeski, Adam W.  Incel, James J.  Incel, James J.  Incel, James J.  Incel, James J.  Intro. PROCESS FOR THE PREPARATION OF RESIN-BOUND  INTON: PEPTIDES  CATION NUMBER: US/09/442,989  G DATE: 1998-11-18  G DATE: 1998-04-15  G DATE: 1998-04-15  Intro. Ser (0.81,897  Intro. Ser (0.81,897  ATION: EMOC-Ala  PTIDE  ATION: Ser (0.81)  PTIDE  ATION: Glu (0.8u)  PTIDE  ATION: Glu (0.8u)  PTIDE  ATION: Glu (0.8u)  PTIDE  ATION: Glu (1.xt)  PTIDE  ATION: His (Trt)  PTIDE  ATION: His (Trt)  PTIDE  ATION: Mae (Trt)  ATION: Nee                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | GENERAL I   | NFORMATION: |                       |                |
| DATE: Janes J. WINTON: PROCESS FOR THE PREPARATION OF RESIN-BOUND NUTION: PROCESS FOR THE PREPARATION OF RESIN-BOUND NUTION: PROTEIDES CATION NUMBER: US/09/442,989 CATION NUMBER: 60/081,897 CATION Set (obs.) PTIDE DATION: FMOC-Ala PTIDE DATION: Glu (obs.) PTIDE ATION: Glu (ots.) PTIDE DATION: His (Trt) PTIDE ATION: His (Trt) PTIDE ATION: Ms (Trt)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | APPLICAN    | T: Sledeski | Adam                  |                |
| WILLOW: FROCESS FOR THE FREFARALION OF RESIN-BOUND WITLOW: PREPTIES E. A3112B-US CATION NUMBER: US/09/442,989 CATION NUMBER: 60/081,897 G DATE: 1998-04-15 G DATE: 1998-04-15 G DATE: 1998-04-15 G DATE: 1908-04-15 G DATE: 19 | AFFLICAN    | T: Mencel,  | AMES U.               | digitor of the |
| E: A3113B-US CATION NUMBER: G DATE: 1998-04 G DATE: 1998-04 I ID NOS: 46 entin Ver. 2.1 tificial Sequer PTIDE PTID | TITIE OF    | INVENTION   | FOR THE PREPARALION   | KESTIN-BOOME   |
| CATION NUMBER: G DATE: 1999-10 G DATE: 1998-104 ID NOS: 46 entin Ver. 2.1 tificial Sequer FIDE ATION: FMOC-Ale PTIDE ) ATION: Ser (OLBU PTIDE ) ATION: Glu (OLBU PTIDE ) ATION: Glu (Trt) PTIDE ) ATION: His (Trt) PTIDE ) ATION: His (Trt) PTIDE ) ATION: His (Trt) D_RES ) D_RES ) ATION: Nie                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | FILE REF    | ERENCE: A31 | 13B-US                | ,              |
| G DATE: 1999-11 CATION NUMBER: G DATE: 1998-04 Entin Ver. 2.1  tificial Sequer FTIDE ATION: FMOC-Ale PTIDE ATION: Ser (OLBU PTIDE ATION: Glu (OLBU PTIDE ATION: Glu (Trt) PTIDE ATION: His (Trt) PTIDE ATION: His (Trt) PTIDE ATION: His Asn (Trt) D_RES ATION: Nle                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | CURRENT     | APPLICATION | NUMBER: US/09/442,989 |                |
| BARLIER APPLICATION NUMBER: 66/081,897  BARLIER FILING DATE: 1998-04-15  SEQ ID NO 3146  SEQ ID NO 3146  LENGTH: 12  TYPE: PRT  ORGANISM: Artificial Sequence FEATURE:  LOCATION: (1)  OTHER INFORMATION: FMOC-Ala  FEATURE:  NAME/KEY: PEPTIDE  LOCATION: (3)  OTHER INFORMATION: Ser (OLBU)  FEATURE:  NAME/KEY: PEPTIDE  LOCATION: (4)  OTHER INFORMATION: Glu (OLBU)  FEATURE:  NAME/KEY: PEPTIDE  LOCATION: (6)  OTHER INFORMATION: Glu (OLBU)  FEATURE:  NAME/KEY: PEPTIDE  LOCATION: (6)  OTHER INFORMATION: His (Trt)  FEATURE:  NAME/KEY: PEPTIDE  LOCATION: (6)  OTHER INFORMATION: His (Trt)  FEATURE:  NAME/KEY: PEPTIDE  LOCATION: (9)  OTHER INFORMATION: Asn (Trt)  FEATURE:  NAME/KEY: MOD_RES  LOCATION: (10)  OTHER INFORMATION: Nie                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | CURRENT     | FILING DATE | : 1999-11-18          |                |
| BARLIER FILING DATE: 1998-04-15 SOFTWARE OF EZQ ID NOS: 46 SOFTWARE PATENT VERY. 2.1 SEQ ID NO 31 LENGTH: 12 TYPE: PRT ORGANISM: Artificial Sequence FEATURE: NAME/KEY: PEPTIDE LOCATION: (1) OTHER INFORMATION: FMOC-Ala FEATURE: NAME/KEY: PEPTIDE LOCATION: (3) OTHER INFORMATION: Ser (OtBu) FEATURE: NAME/KEY: PEPTIDE LOCATION: (4) COTHER INFORMATION: Glu (OtBu) FEATURE: NAME/KEY: PEPTIDE LOCATION: (6) OTHER INFORMATION: Glu (OtBu) FEATURE: NAME/KEY: PEPTIDE LOCATION: (6) OTHER INFORMATION: His (Trt) FEATURE: NAME/KEY: PEPTIDE LOCATION: (9) OTHER INFORMATION: His (Trt) FEATURE: NAME/KEY: PEPTIDE LOCATION: (9) OTHER INFORMATION: Asn (Trt) FEATURE: NAME/KEY: PEPTIDE LOCATION: (10) OTHER INFORMATION: Nie                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |             | APPLICATION | NUMBER: 60/081,897    |                |
| NUMBER OF SEQ ID NOS: 46  SEQ ID NO 31  LENGTH: 12  THE: PRT ORGANISM: Artificial Sequence FRATURE: NAME/KEY: PEPTIDE LOCATION: (1) OTHER INFORMATION: FMOC-Ala FRATURE: NAME/KEY: PEPTIDE LOCATION: (3) OTHER INFORMATION: Ser (OtBu) FRATURE: NAME/KEY: PEPTIDE LOCATION: (4) OTHER INFORMATION: Glu (OtBu) FRATURE: NAME/KEY: PEPTIDE LOCATION: (4) OTHER INFORMATION: Glu (OtBu) FRATURE: NAME/KEY: PEPTIDE LOCATION: (6) OTHER INFORMATION: His (Trt) FRATURE: NAME/KEY: PEPTIDE LOCATION: (6) OTHER INFORMATION: His (Trt) FRATURE: NAME/KEY: PEPTIDE LOCATION: (10) OTHER INFORMATION: Asn (Trt) FRATURE: NAME/KEY: PEPTIDE LOCATION: (10) OTHER INFORMATION: Asn (Trt) FRATURE: NAME/KEY: MOD_RES LOCATION: (8) OTHER INFORMATION: Nie                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | EARLIER     | FILING DATE | : 1998-04-15          |                |
| entin Ve: tificial PTIDE ATION: FP PTIDE ATION: Gl ATION: Gl PTIDE ATION: Gl PTIDE ATION: Hi PTIDE ATION: Hi PTIDE ATION: Hi ATION: Hi ATION: Hi ATION: Hi ATION: Hi ATION: AS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | NUMBER O    | F SEQ ID NO | S: 46                 |                |
| tificial PTIDE ATION: FP PTIDE PTIDE PTIDE PTIDE ATION: Gl PTIDE ATION: Hi PTIDE ATION: Hi ATION: Hi ATION: Hi ATION: Hi ATION: Hi ATION: AB                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | SOFTWARE    |             |                       |                |
| tificial  PTIDE  ATION: FP PTIDE  PTIDE  PTIDE  PTIDE  PTIDE  PTIDE  PTIDE  ATION: Gl  ATION: Hi PTIDE  ATION: AS  ATION: AS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | SEO ID NO   | 31          |                       |                |
| tificial PTIDE ATION: FP PTIDE ATION: Se PTIDE DATION: Gl ATION: Gl ATION: Hi PTIDE ATION: Hi PTIDE DATION: Hi PTIDE DATION: Hi ATION: AE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | LENGIH:     | 12          |                       |                |
| PTIDE ) ATION: FP PTIDE ) ATION: Se PTIDE ) ATION: Gl ATION: Gl PTIDE ) ATION: Hi PTIDE ) ATION: Hi D ATION: Hi ATION: Hi ATION: Hi ATION: AB                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | TYPE: P     |             |                       |                |
| PTIDE  ATION: FP PTIDE  PTIDE  PTIDE  ATION: Gl ATION: Gl ATION: Hi PTIDE  ATION: AE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | ORGANIS     |             |                       |                |
| ATION: PTIDE ATION:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | FEATURE     |             |                       |                |
| ) ATION: PTIDE PTIDE PTIDE PTIDE ATION: PTIDE ATION: PTIDE ATION: ATION: ATION: ATION: ATION: ATION: ATION: ATION: ATION:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | NAME/KE     |             |                       |                |
| PTIDE ) PTIDE ()                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | LOCATIO     | N: (1)      |                       |                |
| PTIDE ATION: PTIDE ATION: PTIDE ATION: PTIDE ATION: PTIDE ATION: PTIDE ATION: DD BTIDE ATION: ATION: ATION: ATION:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | OTHER I     | NFORMATION: | FMOC-Ala              |                |
| PTIDE ATION: PTIDE ATION: PTIDE ATION: ATION: PTIDE O) ATION:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | FEATURE     |             |                       |                |
| PTIDE DATION: PTIDE DATION: PTIDE DATION: PTIDE DATION: PTIDE DATION: PTIDE DATION: ATION: ATION: ATION: ATION:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | NAME/KE     |             |                       |                |
| PTIDE ) ATION: PTIDE ) ATION: PTIDE ) ATION: PTIDE () ATION: D) ATION: ATION: ATION: ATION: ATION:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | COCATIO     | N: (3)      |                       |                |
| PTIDE  ATION: PTIDE  PTIDE  ATION: PTIDE  ATION: PTIDE  OTION: ATION: ATION: ATION: ATION: ATION: ATION:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | OTHER I     | NFORMATION: |                       |                |
| PTIDE ATION:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | FEATURE     |             |                       |                |
| PTIDE  PTIDE  ATION: PTIDE  ATION: ATION: ATION: ATION: ATION: ATION:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | NAME/KE     |             |                       |                |
| PTION:  PTIDE  ATION:  PTIDE  PTIDE  O)  ATION:  ATION:  ATION:  ATION:  ATION:  ATION:  ATION:  ATION:  ATION:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | LOCATIO     | N: (4)      |                       |                |
| PTIDE ) ATION: PTIDE ) ATION: PTIDE 0) ATION: PTIDE 0) ATION:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | OTHER I     | NFORMATION: | Glu (OtBu)            |                |
| PTIDE ) ATION: PTIDE ) ATION: O) ATION: ATION: ATION: ATION:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | FEATURE     |             |                       |                |
| ATION: PTIDE ) ATION: PTIDE 0) ATION: ATION: ATION:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | NAME/KE     |             |                       |                |
| PTIDE ) ATION: PTIDE 0) ATION: D_RES ATION:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | LOCATIO     | N: (6)      |                       |                |
| PTIDE ) ATION: PTIDE 0) ATION: D_RES ) ATION:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | OTHER I     | NFORMATION: |                       |                |
| PTIDE ) ATION: PTIDE 0) ATION: D_RES ) ATION:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | FEATURE     |             |                       |                |
| ATION: PTIDE 0) ATION: ATION: D_RES ) ATION:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | NAME/KE     |             |                       |                |
| ATION: 0) ATION: D_RES 7 ATION:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | LOCATIO     |             |                       |                |
| PTIDE 0) ATION: D_RES )-RES ATION:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | OTHER I     | NFORMATION: | His (Trt)             |                |
| PTIDE 0) ATION: D_RES ) ATION:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | FEATURE     |             |                       |                |
| O)<br>ATION:<br>D_RES<br>)-ATION:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | NAME/KE     |             |                       | -              |
| ATION: D_RES ) ATION:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | LOCATIO     |             |                       |                |
| FEATURE: NAME/KEY: MOD_RES LOCATION: (8) OTHER INFORMATION: Nle                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | OTHER I     | NFORMATION: | Asn(Trt)              |                |
| NAME/KEY: MOD_RES<br>LOCATION: (8)—<br>OTHER INPORMATION: NIe                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | FEATURE     |             |                       |                |
| LOCATION: (8) OTHER INFORMATION: Nle                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | NAME/KE     | Y: MOD RES  |                       |                |
| OTHER INFORMATION: NIE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | LOCATIO     | N: (8)      |                       |                |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | OTHER       | NFORMATION: | Nle                   |                |

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TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid FILE REPERBNCE: 0609.4570001

CURRENT APPLICATION NUMBER: US/09/421,379

CURRENT FILING DATE: 1999-10-20

EARLIER APPLICATION NUMBER: U.S. 60/105,530

EARLIER APPLICATION NUMBER: U.S. 60/105,530

NUMBER OF SEQ ID NOS: 138

SOFTWARE: Patentin Ver. 2.0
 FEATURE:
GOTHER INFORMATION: Description of Artificial Sequence: synthetic
GOTHER INFORMATION: peptide
18-09-421-379-6
 1; Indels
 Length 9;
 APPLICANT: Adermann, Knut
APPLICANT: Adermann, Knut
APPLICANT: Hock, Dieter
APPLICANT: Mackes
TITLE OF INVENTION: Peptides from the hPTH Sequence
NUMBER OF SEQUENCES: 36
CORRESSONDENCE ADDRESS:
ADDRESSEB: JOHNS & ASKew, LLP
STREET: 191 Peachtree Street, 37th Floor
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/817,547A
 63.9%; Score 39; DB 4;
88.9%; Pred. No. 3e+05;
tive 0; Mismatches
 FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P194
APTORNEY/AGENT INFORMATION:
NAME: FROST, ROCER T.
REGISTRATION NUMBER: 22,176
REFERENCE/DOCKET NUMBER: 07826-0007
TELECOMMUNICATION INFORMATION:
 07826-0007
 COMPUTER READABLE FORM:
WIDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 ; Sequence 2, Application US/08817547A ; Patent No. 6030790
 TYPE: PRT
ORGANISM: Artificial Sequence
 INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
 TELEPHONE: 404-818-3700
 Query Match
Best Local Similarity 88.9
Matches 8; Conservative
 404-818-3799
 STRANDEDNESS: unknown TOPOLOGY: unknown
 MOLECULE TYPE: peptide
HYPOTHBTICAL: no
ANTI-SENSE: no
US-08-817-547A-2
 amino acid
 1 AVSEIQFMH
 1 AVSEIQLMH
 GENERAL INFORMATION:
 Georgia
 CITY: Atlanta
 30303
 RESULT 4
US-08-817-547A-2
 TELEFAX:
 COUNTRY:
 STATE:
 SEQ ID NO 6
LENGTH: 9
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; DB 4; hems.
 68.9%; Score 42; DB 3; Length 10; 80.0%; Pred. No. 0.06; Live 1; Mismatches 1; Indels
 Sequence 1, Application US/08817547A
Patent No. 6030790
GENERAL INFORMATION:
APPLICANT: Adermann, Knut
APPLICANT: Magerlein, Markus
TITLE OF INVENTION: Peptides from the hPTH Sequence
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew, LLP
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,547A
 ADDRESSEE: Jones & Askew, LLP
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
 Score 49; DB Pred. No. 0.000; Mismatches
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/03757
FILING DATE: 29 SEPT 1994
ATTORNEY/AGENT INFORMATION:
NAME: FROST, ROGER T.
REGISTRATION NUMBER: 22,176
REFERENCE/DOCKET NUMBER: 07826-0007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
 US-00-421-379-6; Sequence 6, Application US/09421379; Sequence 6, Application US/09421379; Patent No. 6495662; GENERAL INPORMATION: APPLICANT: Kronenberg, Henry; APPLICANT: Pottes, John T. APPLICANT: Pottes, John T. APPLICANT: Pottes, John T. APPLICANT: Juppner, Harald
 TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
 80.3%;
 10 amino acids
 Query Match
Best Local Similarity 80.0
Matches 8; Conservative
 unknown
 10; Conservative
 1 AVSEIGFMHNLG 12
 1 AVSEIQLXHNLG 12
 MOLECULE TYPE: peptide HYPOTHETICAL: no
 1 AVSEIQFMHN 10
 1 SVSEIOLMHN 10
 unknown
 amino acid
 Query Match
Best Local Similarity
Matches 10; Conserv
 Georgia
: USA
 STRANDEDNESS:
 FILING DATE:
 RESULT 2
US-08-817-547A-1
 STATE: GOUNTRY:
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1 AVSEHOLEHN 10

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 US-00-421-379-8

US-00-421-379-8

US-00-421-379-8

US-00-421-379-8

Paquence 8, Application US/09421379

Paquence 8, Application US/09421379

Patent No. 649562

GENERAL INPORMATION:

APPLICANT: Gardella, Thomas J.

APPLICANT: Gardella, Thomas J.

APPLICANT: Gardella, Thomas J.

APPLICANT: Gardella, Thomas J.

APPLICANT: Juppner, Harald

ITILE OF INVENTION: Broactive Peptides and Peptide Derivatives of

ITILE OF INVENTION: Broactive Peptides (PTH) and Parathyroid

ITILE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid

ITILE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid

CURRENT APPLICATION NUMBER: US/09/421,379

CURRENT FILING DATE: 1999-10-22

MUMBER OF EQU IN NOS: 13

SOFTWARE: PatentIn Ver. 2.0

FAMILY SEQ ID NOS: 13

SEQ ID NOS

FAMILY PARAMER: PatentIn Ver. 2.0
) OTHER INFORMATION: Description of Artificial Sequence: synthetic; OTHER INFORMATION: peptide US-09-421-379-8
 .
0
 Sequence 42, Application US/08140137A
| Patent No. 2817617
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: TUOMANEN, ELAINE
| APPLICANT: TUOMANEN, ELAINE
| TITLE OF INVENTION: ANALOGS OF ENDOTHELIAL LEUKOCYTE
| TITLE OF INVENTION: ADHESION MOLECULE (ELAM)
| NUMBER OF SEQUENCES: 49
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: ALBUDER & Jackson STREET: 411 Hackensack Avenue
| CITY: Hackensack STATE: New Jersey
| COUNTRY: USA
 Ouery Match
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 6; Conservative 1; Mismatches 2; Indels
 COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PACHOLING-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/140,137A
FILING DATE: 27-MAY-1994
CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
NAME: Jackson Eq., David A.
REGISTRATION NUMBER: 26,742
REFRENCE/DOCKET NUMBER: 600-1-096
TELECOMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
 ORGANISM: Artificial Sequence
 1 AVSEIOFMH
 1 AVSEHOLLH
 ZIP: 07601
 US-08-140-137A-42
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 0;
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 Gaps
 Gaps
 Sequence 7, Application US/09421379;
Patent No. 649562
GENERAL INFORMATION:
APPLICANT: Gardella, Thomas J.
APPLICANT: Gardella, Thomas J.
APPLICANT: Focts, John T.
APPLICANT: Potts, John T.
TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of TITLE OF INVENTION: Bioactive Peptide (PTH) and Parathyroid TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid TITLE REFERENCE: 0609.4570001;
CURRENT APPLICATION NUMBER: US/09/421,379
CURRENT RILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: U.S. 60/105,530
EARLIER PILING DATE: 1998-10-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 7
LENGTH: 9
 .0
 CTHER INFORMATION: Description of Artificial Sequence: synthetic // OTHER INFORMATION: peptide US-09-421-379-7
 ó.
 Query Match 50.8%; Score 31; DB 6; Length 11; Best Local Similarity 70.0%; Pred. No. 8.5; Matches 7; Conservative 0; Mismatches 3; Indels
 1; Indels
 Score 36; DB 3; Length 9;
Pred. No. 3e+05;
1; Mismatches 1; Indels
 Query Match 59.0%; Score 36; DB 4; Length 9; Best Local Similarity 77.8%; Pred. No. 3e+05; Matches 7; Conservative 1; Mismatches 1; Indels
 RESULT 6
5460978-3
; PACENT NO. 5460978
; PRUCANT: MARTIN, THOMAS J.; MOSELEY, JANE M.; KEMP,
; BRUCE E.; WETTENHALL, RICHARD E.H.
; HYPERCALCEMIE OF INVENTION: PROTEIN ACTIVE IN HUMORAL
; HYPERCALCEMIE OF MALIGNANCY-PTHRP
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/715,280
; FILING DATE: 14-UTW-1991
; APPLICATION NUMBER: 199,235
; FILING DATE: 09-MAY-1988
; FILING DATE: 09-MAY-1988
; FILING DATE: 09-MAY-1988
 59.0%;
 TYPE: PRT (ORGANISM: Artificial Sequence
Query Match
Best Local Similarity 77.8
Matches 7; Conservative
 1 AVSEIQFMHN 10
 1 SVSEIOLMH 9
 1 AVSEIQFMH 9
 1 AVSEIQLLH 9
 1 AVSEIQEMH 9
 FILING DATE:
 ;
SEQ ID NO:3:
: LENGTH: 11
 US-09-421-379-7
 5460978-3
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RESULT 11
US-08-482-528-42
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0
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0
 Query Match 47.5%; Score 29; DB 2; Length 12; Best Local Similarity 62.5%; Pred. No. 22; Matches 5; Conservative 2; Mismatches 1; Indels
 45.9%; Score 28; DB 3; Length 8; 75.0%; Pred. No. 3e+05; tive 1; Mismatches 1; Indels
 Sequence 3, Application US/08817547A

Sequence 3, Application US/08817547A

Sequence 3, Application US/08817547A

GENERAL INFORMATION:
APPLICANT: Adermann, Knut
APPLICANT: Magerlein, Markus
ITLE OF INVENTION: Peptides from the hPTH Sequence
NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew, LLP
STREET: 191 Peachtree Street, 37th Floor
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,547A
 T: 191 Peachtree Street, 37th Floor
Atlanta
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/03757
FILING DATE: 29 SEPT 1994
ATTORNEY/AGENT INFORMATION:
NAME: FROST, ROGER T.
REGISTRATION NUMBER: 22,176
REFERENCE/DOCKET NUMBER: 07826-0007
TELECOMMINICATION INFORMATION:
TELEPHONE: 404-818-3700
 MOLECULE TYPE: peptide
DESCRIPTION: CaRD peptide segence
 12 amino acids
 TELEFAX: 404-818-3799
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
 Query Match
Best Local Similarity 75.0
Matches 6; Conservative
TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 :|| ||:|
5 ISEEQFVH 12
 unknown
 2 VSEIQFWH 9
 amino acid
 linear
 Georgia
 ; ANTI-SENSE: no
US-08-817-547A-3
 TOPOLOGY: un|
MOLECULE TYPE:
 FILING DATE:
 US-08-140-137A-42
 RESULT 9
US-08-817-547A-3
 TOPOLOGY:
 COUNTRY:
 LENGTH:
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Sequence 9, Application US/08438562; Patent No. 5874255; GENERAL INFORMATION:
 41.0%;
 TELEPHONE: (703)816-4000
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
 44.48;
 Query Match
Best Local Similarity 44.4
Matches 4; Conservative
 MOLECULE TYPE: peptide
 2 ASSSVSYMH 10
 1 AVSEIQEMH 9
 amino acid
 CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
 TOPOLOGY:
 US-08-116-778E-9
 US-08-438-562-9
 RESULT 14
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 ô
 Gaps
 US-09-421-379-10

Sequence 10, Application US/09421379

Patent No. 6495662

GENERAL INFORMATION:

APPLICANT: Gardella, Thomas J.

APPLICANT: Gardella, Thomas J.

APPLICANT: Stroneberg, Henry

APPLICANT: Stroneberg, Henry

APPLICANT: Duppner, Harald

ITILE OF INVENTION: Bloactive Peptides and Peptide Derivatives of

ITILE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid

ITILE OF INVENTION: Hormone-Related Peptide (PTH:P)

FILE REFERENCE: 0609,4570001

CURRENT APPLICATION NUMBER: US/09/421,379

CURRENT FILING DATE: 1999-10-20

SARLIER FILING DATE: 1999-10-22

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 10

LENGTH: 9
) OTHER INFORMATION: Description of Artificial Sequence: synthetic; CTHER INFORMATION: peptide
US-09-421-379-10
 ..
 ..
 44.3%; Score 27; DB 3; Length 12; 55.6%; Pred. No. 54; ative 1; Mismatches 3; Indels
 Indels
 42.6%; Score 26; DB 4; Length 9; 55.6%; Pred. No. 3e+05; tive 2; Mismatches 2; Indels
 COUNTRY: USA
ZIP: 92713-5210
COMPUTER ERAABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: TEM PC compatible
COMPUTER:
 ORGANISM: Artificial Sequence FEATURE:
 Query Match
Best Local Similarity 55.6
Matches 5; Conservative
 Query Match
Best Local Similarity 55.6
Matches 5, Conservative
 MOLECULE TYPE: peptide
 3 ASSSVTFMH 11
 1 AVSEIQEMH 9
California
 1 AVSEIQFMH 9
 : | | | : | svsehQllh 9
 US-08-482-528-42
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Gaps
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0
 Score 25, DB 2; Length 10;
Pred. No. 1.1e+02;
2; Mismatches 3; Indels
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAL, NOBUO
APPLICANT: HANAL, NOSHHHISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERYYE P.C.
STREET: 1100 NORTH GLEBE ROAD
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 Length 10;
 Query Match
Best Local Similarity 44.4%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 3; Indels
 SIGNE: VICTIVE:
CONTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATICATION NUMBER: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/483,528B
FILING DATE: 07-JUN-95
CLASSIFICATION: 536
TELEPHONE: (703)816-4100
TELEPHONE: (703)816-4100
TELEPHONE: (703)816-4100
TELEPHONE: (703)816-4100
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SUFWARE: Patentin Release #1.0, Version #1.25
CURSTAIN APPLICATION NUMBER: US/08/438,562
FILING DATE: 10-MAY-95
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: 08/116,778
FILING DATE: 07-SEP-93
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WILSOW, WARY J.
REGISTRATION NUMBER: 32,955
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET UNBER: 249-76
TELEPHONE: (703)816-4000
 RESULT 15
UG-08-483-528B-97
is Sequence 97, Application US/08483528B
is patent No. 5939532
is GENERAL INFORMATION:
APPLICANT: NAZAWURA, KAZUYASU
APPLICANT: SHITARA, KENYA
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, VOBUO
APPLICANT: HANAI, VOBUO
APPLICANT: HANAI, VOBUO
APPLICANT: HANSIGNAN, WORNO
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: 103
CORRESPONDENCE ADDRESS:
ADDRESSED: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
 TELECURIOLE: (703) 816-100
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENOTH: 10 amino acids
TYPE: amino acid
TYPE: amino acid
 TOPOLOGY: linear;
MOLECULE TYPE: peptide
US-08-438-562-9
 2 ASSSVSYMH 10
 1 AVSEIQFMH 9
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Gaps
 .;
0
 Query Match

41.0%; Score 25; DB 2; Length 10;
Best Local Similarity 44.4%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 3; Indels
 Search completed: September 5, 2004, 09:38:33
Job time : 11 secs
; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-483-528B-97
 2 ASSSVSYMH 10
 1 AVSEIQFMH 9
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